

RESULT 2
US-60-391-781-685
; Sequence 685, Application US/60391781

```
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C.
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Oil in Plants
; FILE REFERENCE: 38-77(52900)B
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/365,301
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 3034
; SEQ ID NO 685
; LENGTH: 3144
; TYPE: DNA
; ORGANISM: Zea mays
US-60-391-781-685

Query Match          10.6%; Score 105.8; DB 8; Length 3144;
Best Local Similarity 81.9%; Pred. No. 3.6e-15;
Matches 122; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 313 caggaaacgaagataatcatatgcttaatttagggatgaggtgtgtgcgaagaat1aa 372
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1245 ccggaaccaaagataataatcatatgcttaactccaagatgaggtgtgtcccaagaat1aa 1304
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 373 aggcttgatatacaatgcatgcatgataatgcatccaggaagcatcatatgcaagc 432
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1305 aagcttgatatacaatgcatgcatgataatgcatccaggaagcatcatatgcaagc 1364
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 433 ttgggtatcacaatcatcttttttc 461
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1365 ttgggtatcacaatcatcttttttc 1393
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-60-391-781-709
; Sequence 709, Application US/60391781
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C.
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Oil in Plants
; FILE REFERENCE: 38-77(52900)B
; CURRENT APPLICATION NUMBER: US/60/391,781
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/365,301
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 3034
; SEQ ID NO 709
; LENGTH: 2919
; TYPE: DNA
; ORGANISM: Zea mays
US-60-391-781-709

Query Match          10.1%; Score 100.8; DB 8; Length 2919;
Best Local Similarity 57.4%; Pred. No. 5.4e-14;
Matches 201; Conservative 0; Mismatches 147; Indels 2; Gaps 1;
```

```
DB 1096 gaataaaaaacttgatatacatgcatgcatgaataatgcaatccaagagcactcatatt 1155
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 425 atgcaagcttgggtattccacaatccattttttctgtataactctt 474
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1156 atggaagcttggatataccatgtaacttaatttttttcgccaagtatgctt 1205
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-60-368-387-1
; Sequence 1, Application US/60368387
; GENERAL INFORMATION:
; APPLICANT: Pearlstein, Richard W.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Hines, Christopher F.
; TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose
; FILE REFERENCE: BRL510PRV
; CURRENT APPLICATION NUMBER: US/60/368,387
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2443
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(2443)
; OTHER INFORMATION: SBEII modified region
US-60-368-387-1

Query Match          9.0%; Score 90.4; DB 8; Length 2443;
Best Local Similarity 58.2%; Pred. No. 1.5e-11;
Matches 178; Conservative 0; Mismatches 126; Indels 2; Gaps 1;

QY 127 attctcgagcgatccaanaacttcattgtctctgagtgtagtctgactgcatgagatctcc 186
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 712 ataccocatcaggaataaagattccaactccagctcgatcaagtaactcaatgagcgagccc 771
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 187 cattatgaagaagatat--agtttaattcttgaactactcttggaacttgagcttgag 244
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 772 caggagaataacatcatgattgattatgactcccttcgaagaggaatgagatgagt 831
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 245 gcatgcataatatactatcatcaacttaagatagagatgcatgcaatttgatg 304
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 832 tcaggcatgcatgaacttaacgaacccaataatcatctgcatatataatgaacacatgctcgaa 891
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 305 atcttgacacaggaacogaagaatataatcatatgctaatttagggatgagtggtgcgaa 364
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 892 tgagtagcccggaaccgaagataaacacataatgtaacttttaggtgagatgctcccca 951
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 365 gaataaaagcttggatatacatgcatgcatgcatatgcatccaagagcatctatct 424
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 952 gaataaaanaacttggatatacatgcatgcatgcatataatggaatccaagagcactcatatt 1011
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 425 atgcga 430
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1012 atgcga 1017
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
US-60-381-534-1
; Sequence 1, Application US/60381534
; GENERAL INFORMATION:
; APPLICANT: Pearlstein, Richard W.
; APPLICANT: Broglie, Karen E.
; APPLICANT: Hines, Christopher F.
; TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose
; FILE REFERENCE: BRL510PRV
; CURRENT APPLICATION NUMBER: US/60/381,534
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 6
```

```

: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
:
: LENGTH: 2443
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)_(2443)
:
: OTHER INFORMATION: SBEdit modified region
:
: US-60-381-534-1

```

Query Match	9.0%	Score 90.4	DB 8	Length 2443
Best Local Similarity	58.2%	Pred. No. 1.5e+11		
Matches 178, Conservative	0	Mismatches 126	Indels 2	Gaps 1

[illegible]

```

1      RESULT      6
2      US-10-056-454A-17
3      ; Sequence 17, Application US/10056454A
4      ; GENERAL INFORMATION:
5      ; APPLICANT: National Starch and Chemical Investment Holding Corporation
6      ; TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
7      ; NUMBER OF SEQUENCES: 20
8      ; CORRESPONDENCE ADDRESSES:
9      ; ADDRESSSEE: National Starch and Chemical Investment Holding Corporation
10     ; STREET: 1000 Unidigma Blvd.
11     ; CITY: Newcastle
12     ; STATE: Delaware
13     ; COUNTRY: United States of America
14     ; ZIP: 19720
15     ; COMPUTER READABLE FORM:
16     ; MEDIUM TYPE: Floppy disk
17     ; COMPUTER: IBM PC compatible
18     ; OPERATING SYSTEM: PC-DOS/MS-DOS
19     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
20     ; CURRENT APPLICATION DATA:
21     ; APPLICATION NUMBER: US/10/056,454A
22     ; FILING DATE: 25-Jun-2002
23     ; INFORMATION FOR SEQ ID NO: 17:
24     ; SEQUENCE CHARACTERISTICS:
25     ; LENGTH: 2529 base pairs
26     ; TYPE: nucleic acid
27     ; STRANDEDNESS: single
28     ; TOPOLOGY: linear
29     ; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
30     ; US-10-056-454A-17

```

Query Match	8.8%	Score 88;	DB 7;	Length 2529;
Best Local Similarity	73.7%;	Pred. No. 5.5e-11;		
Matches 112;	Conservative	0;	Mismatches 40;	Indels 0;
			Gaps	0;

Oy	588	gcctgtccagagtaaccctgtaactaatcttttgaccccaagtagcgcgttttggaaactca	657
Db	1100	gcttgcgttttggttatctcmtgacacaaaatttttttgacacaaagacgcgttttgaaagccgc	1159
Oy	658	gaggacttaaaactccatgcgatagacacatgaagctggttcgtctbctctatgat	717
Db	1160	gagacacctgaagcttttgattgattgaataaagccatgacacctgagaaattgctgtctcattgac	1219
Oy	718	atgtctcattagtaattagtcacaaatthaatt	749
Db	1220	attgtctcacagcccatgcataaataattactt	1251

```

1      RESULT 7
2      US-10-056-454A-16
3      ; Sequence 16, Application US/10056454A
4      ; GENERAL INFORMATION:
5      ; APPLICANT: National starch and Chemical Investment Holding Corporation
6      ; TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
7      ; NUMBER OF SEQUENCES: 20
8      ; CORRESPONDENCE ADDRESSES:
9      ; ADDRESSSEE: National Starch and Chemical Investment Holding Corporation
10     ; STREET: 1000 Uniigma Blvd.
11     ; CITY: Newcastle
12     ; STATE: Delaware
13     ; COUNTRY: United States of America
14     ; ZIP: 19720
15     ; COMPUTER READABLE FORM:
16     ; MEDIUM TYPE: Floppy disk
17     ; COMPUTER: IBM PC compatible
18     ; OPERATING SYSTEM: PC-DOS/MS-DOS
19     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
20     ; CURRENT APPLICATION DATA:
21     ; APPLICATION NUMBER: US/10/056,454A
22     ; FILING DATE: 25-Jun-2002
23     ; INFORMATION FOR SEQ ID NO: 16:
24     ; SEQUENCE CHARACTERISTICS:
25     ; LENGTH: 2576 base pairs
26     ; TYPE: nucleic acid
27     ; STRANDEDNESS: single
28     ; TOPOLOGY: linear
29     ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
30     US-10-056-454A-16

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Query Match          8.8%  Score 88; DB 7; Length 2576;
Best Local Similarity 73.7%; Pred No. 5.5e-11;
Matches 112; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY  598  gctgttcacaggtacacatgttactaaattttttgtcaccaagtagccggttttggaaactcca 657
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   1105  GCTAGTTTGGTTATCATCATCAAAATTTTGTTCACCAAGCAGCGGTTTGGAAAGGCC 1164

QY  658  gaggaactaaatccttgcgtatgataagacacatgaactgttgctgttcttaagat 717
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   1165  GACGACCTTAACCTTTGATGATTAAGCTCAAGACCTAGGAATGTTGTTCCATGAGAC 1224

QY  718  attgttcacagtgtaattagtcacatctaatt 749
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   1225  ATTGTTCAACAGCCATCATCAATAATTAATCTTT 1256

RESULT      8
US-10-056-454A-19
: Sequence 19, Application US/10056454A
:
: GENERAL INFORMATION:
:
: APPLICANT: National Starch and Chemical Investment Holding Corporation
:
: TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
:
: NUMBER OF SEQUENCES: 20

```


GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidema Blvd.
CITY: Newcastle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 3231 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-056-454A-18

Query Match	8.8%	Score 88	DB 7	Length 3231
Best Local Similarity	73.7%	Pred. No. 5.8e-11		
Matches 112	Conservative	0	Mismatches 40	Indels 0
			Gaps	0
QY 598	gctgttcacagatcacatggtctactcaatttttgcaccagtagccgttttgcgaactca	657		
Db 1413	gctagtgttggtttatcagatgcacaaattttttgcaccacagccggttttggaaagcc	1472		
QY 658	gaaggaactaaatcccttgatcgatagagacatgagcttggtttgcgtttcttaattgat	717		
Db 1473	gacagaccttaagcttttgattgattaaagccatgagcttgaagaattggtttctcatggac	1532		
QY 718	atcgttcaataggttaattagtcacaattcaattt	749		
Db 1533	attgtttcacaccatgcattcaataattatctttt	1564		

RESULT 12
 US-10-056-454A-13
 : Sequence 13, Application us/10056454A
 :
 GENERAL INFORMATION:
 APPLICANT: National Starch and Chemical Investment Holding Corporation
 TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: National Starch and Chemical Investment Holding Corporation
 STREET: 1000 Unigema Blvd.
 CITY: Newcastle
 STATE: Delaware
 COUNTRY: United States of America
 ZIP: 19720
 :
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/056,454A
 FILING DATE: 25-Jun-2002
 :
 INFORMATION FOR SEQ. ID NO.: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2975 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

```

;
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-056-454A-13

      TOPOLOGY: linear

Query Match      8.5%; Score 84.8; DB 7; Length 2975;
Best Local Similarity 72.4%; Pred. No. 3.2e-10;
Matches 110; Conservative 0; Mismatches 42; Indels 0; Gaps 0.

Oy 598 gctgtccaggtacatcattactaatctttttgcaccagaatgacgcgtttggaactcca 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1329 GCTAaTTTTTGGTATCAATGTCACAATTTTTTTTGGACCAAGACGCGTTTTGGAAAGCCCC 1388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 658 gaggaacttaaaatccctgatacagatagagacacatgagctgtgtgtcgttctctatbgaat 717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1389 GAGGACCTTAAAGTCTTCATGATGATTAAGGCTCATGAGCTGAGCAATGTGTCTCTCATGAGAC 1448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy 718 attgttcattagtagtaattgctccaatttaatt 749
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1449 ATGCTTCAAGCCATGCATCAATAATATACTTT 1480
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 13
; Sequence 16451, Application us/10219999
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)C
; CURRENT APPLICATION NUMBER: US/10/219, 999
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 16451
; LENGTH: 2324
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(2027)
; OTHER INFORMATION:
; US-10-219-999-16451

```

RESULT 14
US-10-110-777-1
; Sequence 1, Application US/10110777
; GENERAL INFORMATION:

```

1  APPLICANT: National Research Council of Canada
2  APPLICANT: Baga, Monica
3  APPLICANT: Peng, Mingsheng
4  APPLICANT: Nair, Ramesh
5  APPLICANT: Repellin, Anne
6  APPLICANT: Gao, Ming
7  APPLICANT: Hucl, Pierre
8  APPLICANT: Scoles, Graham
9  APPLICANT: Chibbar, Ravindra
10 TITLE OF INVENTION: Starch Branching Enzymes
11 FILE REFERENCE: 45187
12 CURRENT APPLICATION NUMBER: US/10/110,777
13 CURRENT FILING DATE: 2002-04-25
14 PRIOR APPLICATION NUMBER: PCT/CA00/01276
15 PRIOR FILING DATE: 2000-10-27
16 PRIOR APPLICATION NUMBER: US60/162,144
17 PRIOR FILING DATE: 1999-10-29
18 NUMBER OF SEQ ID NOS: 2
19 SOFTWARE: PatentIn Ver. 2.1
20 SEQ ID NO 1
21 LENGTH: 4563
22 TYPE: DNA
23 ORGANISM: Titileum aestivum
24 US-10-110-777-1

```

Query Match	7.1%;	Score 71;	DB 7;	Length 4563;
Best Local Similarity	57.4%;	Pred. No. 6.5e-07;		
Matches 128;	Conservative 0;	Mismatches 95;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 15
PCT-US02-18947-442
Sequence 442, Application PC/TUSO218947
GENERAL INFORMATION:
APPLICANT: Rosetta Inpharmatics
TITLE OF INVENTION: Diagnosis and Prognosis
FILE REFERENCE: 9301-175-228
CURRENT APPLICATION NUMBER: PCT/US02/18947
CURRENT FILING DATE: 2002-06-14
PRIORITY APPLICATION NUMBER: 60/380,770
PRIORITY FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2659
SEQ ID NO 442
LENGTH: 2913
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_000158
DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-442

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Query Match	6.98;	Score 68.8;	DB 1;	Length 2913;
Best Local Similarity	63.1%;	Pred. No. 1.9e-06;		
Matches 106; Conservative	0;	Mismatches 62;	Indels 0;	Gaps 0;

Oy 309 tgaacagaccaggagatnaattcatatgatcttaattttagagatgaggtgtgcagaat 366
 Db 699 ttcccatgaagaaagatgcttcttataaaccatttcatatgcaatgtactaccagaat 756
 Oy 369 taaaggttgcatacaatgycagtgcaagataatgcaatccagagatcatactg 426
 Db 759 caaagctctgatacaactctcatctcaatttgaatgcaatcttgaagatgtctactg 816
 Oy 429 aagcttggatcacacaatcatatctttcttgcatacacttca 476
 Db 819 cagcttctgtaccacaatcatcaagctcttcttgcagcttccagccggtta 866

Search completed: September 12, 2002, 09:13:22
Job time: 11199 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 07:30:52 ; Search time 5258.2 Seconds
(without alignments)
4114.507 Million cell updates/sec

Title: US-09-508-377-10_COPY_1_1000
Perfect score: 1000
Sequence: 1 agaaccctccatttaga.....aacctcccgtygtccct 1000

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

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2: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
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27: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
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29: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
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33: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
34: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
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36: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
37: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
38: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
39: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
40: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
41: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
42: /cgn2_6/pdata/1/pna/US086_COMB.seq:*
43: /cgn2_6/pdata/1/pna/US086_COMB.seq:*

44: /cgn2_6/pdata/1/pna/US6005_COMB.seq:*
45: /cgn2_6/pdata/1/pna/US6006_COMB.seq:*
46: /cgn2_6/pdata/1/pna/US6007_COMB.seq:*
47: /cgn2_6/pdata/1/pna/US6008_COMB.seq:*
48: /cgn2_6/pdata/1/pna/US6009_COMB.seq:*
49: /cgn2_6/pdata/1/pna/US6010_COMB.seq:*
50: /cgn2_6/pdata/1/pna/US6011_COMB.seq:*
51: /cgn2_6/pdata/1/pna/US6012_COMB.seq:*
52: /cgn2_6/pdata/1/pna/US6013_COMB.seq:*
53: /cgn2_6/pdata/1/pna/US6014_COMB.seq:*
54: /cgn2_6/pdata/1/pna/US6015_COMB.seq:*
55: /cgn2_6/pdata/1/pna/US6016_COMB.seq:*
56: /cgn2_6/pdata/1/pna/US6017_COMB.seq:*
57: /cgn2_6/pdata/1/pna/US6018_COMB.seq:*
58: /cgn2_6/pdata/1/pna/US6019_COMB.seq:*
59: /cgn2_6/pdata/1/pna/US6020_COMB.seq:*
60: /cgn2_6/pdata/1/pna/US6021_COMB.seq:*
61: /cgn2_6/pdata/1/pna/US6022_COMB.seq:*
62: /cgn2_6/pdata/1/pna/US6023_COMB.seq:*
63: /cgn2_6/pdata/1/pna/US6024_COMB.seq:*
64: /cgn2_6/pdata/1/pna/US6025_COMB.seq:*
65: /cgn2_6/pdata/1/pna/US6026_COMB.seq:*
66: /cgn2_6/pdata/1/pna/US6027_COMB.seq:*
67: /cgn2_6/pdata/1/pna/US6028_COMB.seq:*
68: /cgn2_6/pdata/1/pna/US6029_COMB.seq:*
69: /cgn2_6/pdata/1/pna/US6030_COMB.seq:*
70: /cgn2_6/pdata/1/pna/US6031_COMB.seq:*
71: /cgn2_6/pdata/1/pna/US6032_COMB.seq:*
72: /cgn2_6/pdata/1/pna/US6033_COMB.seq:*
73: /cgn2_6/pdata/1/pna/US6034_COMB.seq:*
74: /cgn2_6/pdata/1/pna/US6035_COMB.seq:*
75: /cgn2_6/pdata/1/pna/US6036_COMB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1000	100.0	11463	19	US-09-508-377-10	Sequence 10, Appl
2	43.8	4.4	2000	33	US-09-887-272A-5263	Sequence 5263, Ap
3	41.4	4.1	457	31	US-09-824-536-1968	Sequence 1968, Ap
4	41.4	4.1	457	31	US-09-824-628-1968	Sequence 1988, Ap
5	41.4	4.1	623	27	US-09-698-014-36	Sequence 36, Appl
6	41.4	4.1	79976	31	US-09-534-859-818	Sequence 818, App
7	41.4	4.1	79976	31	US-09-803-736-818	Sequence 818, App
8	41.2	4.1	1059	34	US-09-911-345-3	Sequence 3, Appl1
9	40.6	4.1	82356	27	US-09-692-412-73	Sequence 73, Appl
10	40.6	4.1	82356	31	US-09-803-736-1053	Sequence 1053, Ap
11	40.4	4.0	2085	28	US-09-702-134-29670	Sequence 29670, A
12	40.4	4.0	2085	31	US-09-815-264-74236	Sequence 74236, A
13	40.4	4.0	2140	24	US-09-620-392-1096	Sequence 1096, Ap
14	40.4	4.0	3554	24	US-09-702-134-92663	Sequence 9663, Ap
15	40.4	4.0	3554	31	US-09-815-264-86646	Sequence 86646, A
16	40.4	4.0	3808	24	US-09-620-392-45673	Sequence 45673, A
17	40.4	4.0	10079	24	US-09-620-392-26402	Sequence 26402, A
18	40.4	4.0	10079	28	US-09-702-134-24210	Sequence 24210, A
19	40.4	4.0	10079	31	US-09-815-264-67802	Sequence 67802, A
20	39.2	3.9	7218	8	US-08-466-194-14	Sequence 14, Appl
21	39.2	3.9	1055	31	US-09-806-708A-23	Sequence 23, Appl
22	39.2	3.9	32768	60	US-09-612-656-26	Sequence 26, Appl
23	39.2	3.9	832	24	US-09-621-976-2813	Sequence 2813, Ap
24	39.2	3.9	832	53	US-09-147-499-2813	Sequence 2813, Ap
25	39.2	3.9	1169	56	US-09-172-377-2283	Sequence 2283, Ap
26	38.8	3.9	17168	28	US-09-702-134-25673	Sequence 25673, A
27	38.8	3.9	17168	31	US-09-815-264-73103	Sequence 73103, A
28	38.8	3.9	17201	24	US-09-620-392-4351	Sequence 4351, Ap
29	38.2	3.8	2000	33	US-09-887-272A-5263	Sequence 5263, Ap
30	37.8	3.8	712	61	US-09-226-326-6028	Sequence 6028, Ap
31	37.8	3.8	32768	59	US-60-208-129-68	Sequence 68, Appl

32	37.8	3.8	32768	59	US-60-208-873-82	Sequence 82, App
33	37.8	3.8	32768	59	US-60-213-177-192	Sequence 83, App
34	37.8	3.8	32768	60	US-60-233-537-229	Sequence 192, App
35	37.8	3.8	32768	62	US-60-233-537-229	Sequence 239, App
36	37.8	3.8	1141	31	US-09-806-7088-12	Sequence 22, App
37	37.6	3.8	2546	55	US-60-167-217-7239	Sequence 7239, App
38	37.6	3.8	2752	56	US-60-173-464-5758	Sequence 5798, App
39	37.6	3.8	21165	58	US-60-131-637-339923	Sequence 39923, App
40	37.6	3.8	21165	58	US-60-131-681-309930	Sequence 30950, App
41	37.6	3.8	22875	23	US-09-614-150-40282	Sequence 40282, App
42	37.6	3.8	85040	19	US-09-528-237A-922	Sequence 922, App
43	37.4	3.7	290	14	US-09-083-894-2458	Sequence 2458, App
44	37.2	3.7	509	18	US-09-404-549-525	Sequence 525, App
45	37.2	3.7	509	18	US-09-404-549-525	Sequence 525, App

ALIGNMENTS

```

RESULT 1
US-09-508-377-10
Sequence 10, Application US/09508377
GENERAL INFORMATION:
APPLICANT: KALEEN, HONGYILI
APPLICANT: MORELL, MATHEW
APPLICANT: RAHMAN, SADEOUR
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS
FILE REFERENCE: 034270/0126
CURRENT APPLICATION NUMBER: US/09/508,377
CURRENT FILING DATE: 2000-06-09
PRIORITY APPLICATION NUMBER: AU PP 2509
PRIORITY FILING DATE: 1998-03-20
PRIORITY APPLICATION NUMBER: PCT/AU98/00743
PRIORITY FILING DATE: 1998-09-11
PRIORITY APPLICATION NUMBER: AU PP 9108
PRIORITY FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 11463
TYPE: DNA
ORGANISM: Trifolium faucioli
US-09-508-377-10

```

Query Match	100.0%;	Score 1000;	DB 19;	Length 11463;
Best Local Similarity	100.0%;	Pred. No. 2.3e-282;		
Matches 1000;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

QY	361	ttcccccttgtaatttatatgctccacacttttttttaatygaaagcaaggttggcaac	420
Db	361	ttcccccttgyaaattatagctccacacttttttttaatygaaagcaaggttgycaac	420
QY	421	acatgcattttaacaagaaggaatttaatttcaaacacacatatactgaattttcaaa	480
Db	421	acatgcattttcaaacagaaggaatttaatttcaaacacacatatactgaattttcaaa	480
QY	481	ccatgaccgcagcagttccatctgaggttgaaacgaagaactgtaaacatcccaagt	540
Db	481	ccatgaccgcagcagttccatctgaggttgaaacgaagaactgtaaacatcccaagt	540
QY	541	gtcgggtcgaaagaagggatgacactggaagaatgcatatcgattcatattacat	600
Db	541	gtcgggtctgagaagaagggtgacactggaagaatgcatatcgattcatattacat	600
QY	601	gtacacatacataatgtaacctatacaattgttttttggagcagatggtgtgtcttt	660
Db	601	gtacacatacataatgtaacctatacaattgttttttggagcagatggtgtgtcttt	660
QY	661	tttttaacggaataatgcatatgctggtcccgatgctgtgcagatctggatctgtggag	720
Db	661	tttttaacgcgaaatgcatatgctggtcccgatgctgtgcagatctggatctgtggag	720
QY	721	acgaagcgacaatccagacactaccacactgctttgtcttgagacaaataatgtttgt	780
Db	721	acgaagcgacaatccagacactaccacactgctttgtcttgagacaaataatgtttgt	780
QY	781	aaacaaaataaatactataaagcagaggttactagaagcgttaacgcatgtgccaagt	840
Db	781	aaacaaaataaatactataaagcagaggttactagaagcgttaacgcatgtgccaagt	840
QY	841	acggtctcccgccgttgggtttggatctcgctctcccgacagaggttgcctccacg	900
Db	841	acggtctcccgccgttgggtttggatctcgctctcccgacagaggttgcctccacg	900
QY	901	tcgcgtccgtctgcgtccacactctgtgtgtgcggtcgcaagaagggaggaagaacgcg	960
Db	901	tcgcgtccgtctgcgtccacactctgtgtgtgcggtcgcaagaagggaggaagaacgcg	960
QY	961	caacacacatcaacacgcgacactcccgctgggtccct	1000
Db	961	caacacacatcaacacgcgacactcccgctgggtccct	1000

RESULT 2
US-09-887-272A-5263/c
; Sequence 5263, Application US/09887272A

APPLICANT: Hou, Yu-Ming
 APPLICANT: Quan, Sheng
 APPLICANT: Chang, Hur-Song
 APPLICANT: Zhu, Tong
 APPLICANT: Whitlam, Steve
 APPLICANT: Goff, Steve
 APPLICANT: Glazebrook, Jane
 APPLICANT: Chen, Wenguiang
 APPLICANT: Katagiri, Funaki
 APPLICANT: Xie, Zhiyi
 APPLICANT: Tao, Yi
 APPLICANT: Zou, Guangzhou
 APPLICANT: Cooper, Bret
 TITLE OF INVENTION: PLANT GENES INVOLVED IN DEFENSE AGAINST
 TITLE OF INVENTION: PATHOGENS
 FILE REFERENCE: 1360_003052
 CURRENT APPLICATION NUMBER: US/09/887, 272A
 CURRENT FILING DATE: 2001-06-23
 PRIOR APPLICATION NUMBER: 60/213, 634
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: 60/214, 926
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: 60/261, 320
 PRIOR FILING DATE: 2001-01-12

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: PRIOR APPLICATION NUMBER: 60/264,353
:
: PRIOR FILING DATE: 2001-01-26
:
: PRIOR APPLICATION NUMBER: 60/273,879
:
: PRIOR FILING DATE: 2001-03-07
:
: PRIOR APPLICATION NUMBER: 09/887,271
:
: PRIOR FILING DATE: 2001-06-22
:
: NUMBER OF SEQ ID NOS: 6813
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 5263
:
: LENGTH: 2000
:
: TYPE: DNA
:
: ORGANISM: Oryza sativa
:
: OS-09-887-272A-5263

```

Query Match	4.4%	Score 43.8	DB 33	Length 2000
Best Local Similarity	10.2%	Pred. No. 0.37		
Matches 101	Conservative 46	Mismatches 458	Indels 8	Gaps 3

0y	8	ccctcatctttagatcttttttttcttcttcttccttcggaagcgtggtgcgtggaagaattgcgt	67
Db	995	YMTAYSSYTWKMYMYAKMRAVAMSRSSRTTWTGCKRMATYCGTKMVAAGVRRRMAMCW	936
0y	68	cttagtttcttaagaagacagcgcatttagcccttgcttcttaaaagcgaaccagtc	127
Db	935	CCMKMKWMTSCMMWKYKRTYSCWYTWGCMARAYIAMRRRTYTKWSRRMTWTMTKW	876
0y	128	aaaacgtctgtcgaatcacccagcttgcacaagttaaagcgcagacaccacaagaagcgca	187
Db	875	AMTWMTGCMAMKMYMATGMATMTMMWRTYMTYCYAMTCAMCKYKMAMTKMTWTWACMWRA	816
0y	188	ttcgaactgtgacagaagcgtcaagcaggaagcccgaccacaagcgttgagccttgacagcgg	247
Db	815	TSMRRAMAGRMWRKYMKRAY-KWRBWRCKAGAMARMMRSRYKWKKKKATRYTWKMA	757
0y	248	aagctgagcgctgacacatgagcgtcactctatggcgctgcggaagaagaagagacgcac	307
Db	756	MTWMSWRMKSYTKWSSGMRMSANMYCSRMKCATTKTAASSARMTKRAKRSYRRW	697
0y	308	atgaacaccatgatgatgctcgaagcgtgatlggaaggaagacaacatgcacctttcc	367
Db	696	YMKRCGWYRYRYRSCMTFARBSKRRKNAAGASMKSCMYWWRABRMWYSKYSCSAKCC	637
0y	368	tcctggaatctcatcgtccacacttttttctaattgaaagcaagatlggcaacaacatgca	427
Db	636	KKTRMTSSYSTOMYGSSYSYKSMSTYSKMSYGMKTCMYTSMKSTRRSKMGRRSGM	577
0y	428	tttccaacaaggaanaattatcttcaaacacacatgaactgcacatcttcaaacatgca	487
Db	576	SRMTYRMMKKRRKKRYMYMKWCKTMRCKCYRMGYMTYTTSSRMYTARYARYTSKR	517
0y	488	ccgaagcatccatcgtcgaggttgagaagaagacgaagaaatccaactccagttgctgagt	547
Db	516	RYMYWKYKXKCYW-----YYGMYMKSSYMMRYCYCAKCKCCCAKMMKWAHYSMMMYW	462
0y	548	cgagaagaagatgacactgaaagatgacgtatgaattgaattcaatcatcatatgtaca	607
Db	461	RKYSKMMHSTKRYMMSMYWYKCRBSMKYGAKCYCKMMYTCYSGYMKMYWTYMGYSYRC	402
0y	608	tacataaagtacccctacaacttgttttttggagcagaaggtgtgtgctcttttttttac	667
Db	401	YKMYMYYKCMWMTMMYSASSSMMTWYYYAKAKWKYKRRGTMYSYGRSKKKYCTW	342
0y	668	acgaanaagcatatcgtgcgcgcgatcgctgcagatggatgacgtcgtgagaagcag	727
Db	341	CYMKMCRICYRMRKMMRKRTKYSKCYCMRYATCYWCCCYRKRGRYSSRSMMRTAGKKMR	262
0y	728	acaalcagacacatccaactgcttcttctgtcgtgagacacaataatgttttltgtaacaa	787
Db	281	SMSRCSRSYMYKMYKKMKKSYMYSGMARSSGTSWERSAKPTKYGYSYSSRAKMMRAC	222
0y	788	ataatcactttaaagcaggttactagaagccgcgtcaacgcatatgc--caggtaacgc	845

Db	221	RMYSACRRYNTSTYYCGSGYGGSSKKMKMSGCMRHTCSWGSCCYTYTYGAAMCMSCM	162
Qy	846	ctccaccagccgttgglttgcagatctcgtctcccgacgacgagcgtctgcctccaccgtccgt	905
Db	161	SMWYMGSGCGTTRGMKMKMSKYSMCKKCKYCSCTKYCSYTGYYRCKMKYKSYKCYCYC	1020
Qy	906	ccgtctgctgcacactctgtctgtgcgcgcgcacgaagagagaagaaacgcgcgcacac	965
Db	101	YWYMSYMYRMKMKCMCSRFCSGSMSCAYCSTSTSRMMSMYAAAKMGCGSGMYRMKSC	42
Qy	966	acaactacacagcgacacatccccgttggttccc	998
Db	41	KMSYSSCKYTKSGKKCKTKRRYYCYWSSGYM	9

RESULT 3
US-09-824-556-1988
; Sequence 1988, Application US/09824556-
; GENERAL INFORMATION:

```

: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
:
: TITLE OF INVENTION: THEREFOR
:
: FILE REFERENCE: 1600.2084-001
:
: CURRENT APPLICATION NUMBER: US/09/824,556
:
: CURRENT FILING DATE: 2001-04-02
:
: PRIOR APPLICATION NUMBER: US 60/193,423
:
: PRIOR FILING DATE: 2000-03-31
:
: NUMBER OF SEQ ID NOS: 9973
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 1988
:
: LENGTH: 457
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: LOCATION: (1)...(457)
:
: OTHER INFORMATION: n = A,T,C or G
:
US-09-824-556-1988

```

```

Query Match Similarity      4.1%; Score 41.4; DB 31; Length 457;
Best Local Similarity      43.4%; Pred No 0.85;
Matches 75; Conservative 0; Mismatches 98; Indels 0; Gaps 0

Qy 627 ttgttttttgagcagagtgvgtggtcttttttttacgaaatgcatagctcg 686
      ||| |||| | | | | | | | | | | | | | | | | | | | | | | |
Db 136 ttttttttaaaaaaaaagggggggggtttttttttttnnaaaaaaaanctaat 195
      ||| |||| | | | | | | | | | | | | | | | | | | | | | | |

Qy 687 cccgatggtgcagatcgatcgatcggtgcgagagcagcgaatcagacactcacca 746
      ||| |||| | | | | | | | | | | | | | | | | | | | | | | |
Db 196 tttnncccttngncccccgcngngcgggggcnmnnmnnnaaaaaannmta 255
      ||| |||| | | | | | | | | | | | | | | | | | | | | | | |

Qy 747 ctgctttctcgtggagacaataatgttttctgtaacaataataactact 799
      ||| |||| | | | | | | | | | | | | | | | | | | | | | | |
Db 256 annnttttttnncccccggtaaaaaacctttnnncccaaaaaaaattaanat 308
      ||| |||| | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-09-824-628-1988
; Sequence 1988; Application US/09824628
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2084-001
; CURRENT APPLICATION NUMBER: US/09/824, 828
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,423
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9973
; SOFTWARE: FastSeq for Windows Version 4.0

```

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; SEQ ID NO 1988
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(457)
; OTHER INFORMATION: n = A,T,C or G
US-09-824-628-1988
```

```
Query Match          4.1%; Score 41.4; DB 31; Length 457;
Best Local Similarity 43.4%; Pred. NO. 0.85;
Matches 75; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
```

```
OY 627 ttgttttttgagcagagtggtgtgtcttttttttaaccggaataatgcacatgctg 686
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 136 ttttttttaaaaaaaaggggggggttttttttttttttttttttttttttttttt 195
OY 687 ccgcatgctgacatgcagatgcgtgcgagacgacgaatcagacactcacaa 746
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 196 tttnccctttnnccccccnngnngnngnncnnnnnnnnnnnnnnnnnnnnnnnta 255
OY 747 ctgctttgtctggacacataatgttttgaacaaataatattat 799
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 256 annntttttttnnccccgtaaaaacctttnnnccaaaaaaataanaat 308
```

```
RESULT 5
US-09-698-014-36
```

```
; Sequence 36, Application US/09698014
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2014-001
; CURRENT APPLICATION NUMBER: US/09/698,014
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/162,363
; NUMBER OF SEQ ID NOS: 6098
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(623)
; OTHER INFORMATION: n = A,T,C or G
US-09-698-014-36
```

```
Query Match          4.1%; Score 41.4; DB 27; Length 623;
Best Local Similarity 50.2%; Pred. NO. 1;
Matches 102; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
```

```
OY 336 cacccttccctcgtgaatcatagctcacacttttttaatggaagcaggttg 415
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 cccatttcctctctcacttgcttcagcagtgtagtaattcaatgcagaaatg 433
OY 416 caaacatgcttttcaaacagaataatattctcaaccacatgacatgcaatc 475
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 434 gttaacagaacttttcaacaagaagtcacatgacaaatgctccagaattga 493
OY 476 tcaaccatgcgcgacagtcacgagtggaacgaagaactggaataacacatcc 535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 494 tcagataagagcccgcatgttgagattttgggaagaaagactgagttctattcc 553
OY 536 cagttgcagtcgagaagaga 558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
DB 554 cacttctcaattgggagaagga 576
```

```
RESULT 6
US-09-534-859-818
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```
; Sequence 818, Application US/09534859
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Last, Robert L.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: PLANT POLYMORPHIC MARKERS AND USES THEREOF
; FILE REFERENCE: 38-10(15493)B
; CURRENT APPLICATION NUMBER: US/09/534,859
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 1127
; SEQ ID NO 818
; LENGTH: 79976
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-534-859-818
```

```
Query Match          4.1%; Score 41.4; DB 20; Length 79976;
Best Local Similarity 47.8%; Pred. NO. 14;
Matches 120; Conservative 0; Mismatches 131; Indels 0; Gaps 0;
```

```
OY 427 atttcaacaaggaataattctcaaacaccacatgacatgcaattctcaaccatgc 486
    |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 40914 attaatctctgagaatttggtgtatgtctcctcaaatatttaatttagcacac 40973
OY 487 accgacgagtcacatgcaggttggaacgaagaactgaaataacatccagttgcag 546
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 40974 atagacaactatttaagaagatacaacaataattctgctgtaattttagtttaatt 41033
OY 547 ttgagaagaagtgacacacgaagratgctgatactgattcatattacatgataca 606
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 41034 tagagggcaaaaaggcaagaagtaattcttttataatgtatttttaggaagacaat 41093
OY 607 atacatagtacctacaattgttttttgagagagagtggtgtctttttttta 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 41094 atataatgactaataataaagttttttgtctcatcttgattgagtatattatgt 41153
OY 667 cacgaaatgc 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 41154 gaatcaattc 41164
```

```
RESULT 7
```

```
US-09-803-736-818
```

```
; Sequence 818, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 818
; LENGTH: 79976
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
```


OY 428 ttccaacaaggaataatattctcaaacaccctgcacatgcattcttcaaacatgca 487
 Db 43382 TCAACCAAAATTAATATTTATTTCAAAATAGATCAAAATTTTGTGTAACCAAAAT 433223
 OY 488 ccgacagtcacatgcaggtggaaacgaagacatgaaatcaacatc 534
 Db 43322 TTGAATATCTCGAACCAATTTGAACCGAATATCTGAATATTCACATTCG 43276

```

RESULT 11
US-09-702-134-29670/c
: Sequence :29670, Application US/09702134
: GENERAL INFORMATION:
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Cao, tongwei
: APPLICANT: Kovalic, David K.
: APPLICANT: Liu, Jingdong
: APPLICANT: Mcininch, James
: APPLICANT: Wu, Wei
: TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
: FILE REFERENCE: 38-21(51237)F
: CURRENT APPLICATION NUMBER: US/09/702,134
: CURRENT FILING DATE: 2000-10-31
: NUMBER OF SEQ ID NOS: 52202
: SEQ ID NO 29670
: LENGTH: 2065
: TYPE: DNA
: ORGANISM: Oryza sativa
: US-09-702-134-29670

```

Query Match	4.0%	Score 40.4	DB 28	Length 2085
Best Local Similarity	50.5%	Pred. No. 3.8		
Matches 98	Conservative 0	Mismatches 96	Indels 0	Gaps 0
QY 765	caataaactgttttctgtaacaacaaataactataaacgaggtactagagccgctaa	824		
Db 1530	CATCATTTCTGTGTCACATTTAAGTTAATTTGTACAAAAAGAGGCATGAAGCCTTAGA	1471		
QY 825	cggcatgcccaggtaaacgcgtccccagccgttgtttgttgcatcttcgtctccgcgaagc	884		
Db 1470	AGAAAGAAAAAGAAAAAGTTAAGATTGACGGGGGCGCTGGGGGCTCATTTCAACGGGCC	1411		
QY 885	agcgtgcgtccacccgtccgtccgtcgtcgtccacacctctgtctgtgcgcgcgaagaga	944		
Db 1410	AGGTGCGCGGGCGCTGTTGCCACCGTCGGCTTGACATGCTGGCGCTTCCGCCCTGTCGGAG	1351		
QY 945	ggaagaacgaacgc	958		
Db 1350	TGCGGGCGCGAAGCGC	1337		

RESULT 12
US-09-815-264-74236/G
Sequence 74236: Application US/09815264
GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey A.
APPLICANT: Cao, Yongwei
APPLICANT: Dotson, Stewart B.
APPLICANT: Koshi, Jeffrey M.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: McIninch, James
APPLICANT: Wu, Wei
TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31

```

; NUMBER OF SEQ ID NOS: 109569
; SEQ ID NO 74236
; LENGTH: 2085
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-74236

```

Query Match	4.0%;	Score 40.4;	DB 31;	Length 2085;
Best Local Similarity	50.5%;	Pred. No. 3.8;		
Matches 98;	Conservative	0;	Mismatches 96;	Indels 0;
				Gaps 0;

QY	765	caataaatgltttgttaacaaaataaactatataaagaggtactagagcgcceta	824
Db	1350	CATCATTTCTGATGTCGAGATTAACTTAATTTGTACAAAAAAGGCATGAMGGCTTTAGA	1471
QY	825	cgcgcattgcacagtyaaacgcgtccaccgcctgtgtgttcgaactcgtctccgccagac	884
Db	1470	AGAAAGAAAAAGAAAAAGTTAAGATTGGCGGGGGCGCTTGGGGGCTCATTTCTTACCGCGCC	1411
QY	885	agcgtcgcctccacacgcgtccgtccgtcgtgcacccctctgtcgtgcgcgcacgaagga	944
Db	1410	AGGTGCGCGCGGCTGTGGCCACCGTCGCTTGACACTGCTGGCGTTCCCGCCCTCGCGGAG	1351
QY	945	ggaagaacgaacgc	958
Db	1350	TCGGGGGCGGAACGC	1337

```

RESULT 13
US-09-620-392-1096/c
; Sequence 1096, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kowalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 1096
; LENGTH: 2140
; TYPE: DNA
; ORGANISM: Oryza sativa
; OTHER INFORMATION: unsure at all n locations
US-09-620-392-1096

```

	Query Match	4.0%	Score 40.4	DB 24	Length 2140
	Best Local Similarity	50.5%	Pred. No. 3.9		
	Matches 96	Conservative	0	Mismatches 96	Indels 0
				Gaps	
QY	765 caataaaatgtttttaaacaataataactataaacgagtgactagaagccgttaa	824			
Db	1585 CATCATTTTCGATTTCGAGATTAGTTAATTATTGTCACAAAAAAGAGCATGAAAGCCCTTGA	1526			
QY	825 cggcatgtggccaagttaaacgagctcccaagccgtttgtgtttgcgtcttcgcctccgcgaagc	884			
Db	1525 AGAAAGAAAAAGAAAAAGTTAAGATTGGGGGGGGGCGCTGATTCATTCACCGCCGCC	1466			
QY	885 agcgcgcctcccaacgcgtccgtccgtcgcctgcgcacacctctcgttgcgcgcgaagaagga	944			
Db	1465 AGGTGCGCGGGCTCTGTTGCCACCGCTGCTTGCACTGCTTGCGCTTCCCGCCCTGCGTGGAG	1406			
QY	945 ggaagaacgaagcgc	958			
Db	1405 TCGGGCGCGAAGCG	1392			

RESULT 14
US-09-702-134-9663

```
; Sequence 9663, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 9663
; LENGTH: 3554
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-9663
```

```
Query Match 4.0%; Score 40.4; DB 28; Length 3554;
Best Local Similarity 50.5%; Pred. No. 5.1;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 765 caataaatgttttggtaacaataataactataacgaggtactagaagccgctaa 824
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1119 catcattctgtattgtagatgaatgaatatttgacaaaaaagagcatgaagccttaga 1178

QY 825 cggcatggtccaggtaaacgcgcgtccacgcgtgtgtgttcgcatctgtctcccgacgc 884
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1179 agaaagaaaaaagaaagtaaagattgacgaggtgcgtgcctcattctgacgcgcc 1238

QY 885 agcgtgcctccacgcgttcgttcgttcgacccctctgtgcgcgcgcaagaaggga 944
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1239 aggtcgccggcctcgttcgacccgtctgacgtgtgcgttcccccctgtcggag 1298

QY 945 ggaagacgaacgc 958
  | | | | | | |
DB 1299 tcgggggcgaacgc 1312
```

```
RESULT 15
US-09-815-264-86646
; Sequence 86646, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 86646
; LENGTH: 3554
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-86646
```

```
Query Match 4.0%; Score 40.4; DB 31; Length 3554;
Best Local Similarity 50.5%; Pred. No. 5.1;
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
```

```
QY 765 caataaatgttttggtaacaataataactataacgaggtactagaagccgctaa 824
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1119 catcattctgtattgtagatgaatgaatatttgacaaaaaagagcatgaagccttaga 1178

QY 825 cggcatggtccaggtaaacgcgcgtccacgcgtgtgtgttcgcatctgtctcccgacgc 884
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1179 agaaagaaaaaagaaagtaaagattgacgaggtgcgtgcctcattctgacgcgcc 1238

QY 885 agcgtgcctccacgcgttcgttcgttcgacccctctgtgcgcgcgcaagaaggga 944
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1239 aggtcgccggcctcgttcgacccgtctgacgtgtgcgttcccccctgtcggag 1298

QY 945 ggaagacgaacgc 958
  | | | | | | |
DB 1299 tcgggggcgaacgc 1312
```

Search completed: September 12, 2002, 10:08:12
Job time: 9440 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 06:06:43 : Search time 643.61 Seconds
(without alignments)
4916.495 Million cell updates/sec

Title: US-09-508-377-10_COPY_1_1000

Perfect score: 1000

Sequence: 1 agaacacccctccatttaga.....acactcccggtggtccct 1000

Scoring table: IDENTITY_NUC

Searched: 2084544 seqs, 1582152599 residues

Total number of hits satisfying chosen parameters: 4169088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing First 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37.4	3.7	1191139	US-09-811-352B-1	Sequence 1, Appl
2	37.4	3.7	1191139	US-10-140-924-1	Sequence 1, Appl
3	37.4	3.7	1691139	US-10-067-514-1	Sequence 10980, A
4	37.2	3.7	6493	PCT-US02-25766-10980	Sequence 10980, A
5	35.6	3.6	691	US-10-155-881-25269	Sequence 25269, A
6	35.6	3.6	1275	US-10-027-632-213914	Sequence 213914, A
7	35.6	3.6	1741	US-10-201-386-12	Sequence 12, Appl
8	35.4	3.5	2407	US-10-198-846-13552	Sequence 13552, A
9	35.2	3.5	774	US-10-155-881-23995	Sequence 23995, A
10	35	3.5	1754	US-10-155-881-12490	Sequence 12490, A
11	35	3.5	2991	US-10-179-131-2533	Sequence 2533, Ap
12	34.4	3.4	10495	US-09-053-375B-600	Sequence 600, App
13	34.4	3.4	15932	PCT-US02-09105-482	Sequence 482, App
14	34.4	3.4	15932	PCT-US02-09370-1049	Sequence 1049, Ap
15	34.4	3.4	15932	US-10-105-299-6415	Sequence 6415, Ap
16	34.2	3.4	1449	US-10-212-760-275	Sequence 275, App
17	34.2	3.4	1792	US-10-027-632-250431	Sequence 250431, A
18	34	3.4	3422	US-09-979-715-12	Sequence 12, Appl
19	34	3.4	5791	US-09-979-715-13	Sequence 13, Appl
20	33.6	3.4	218336	PCT-US02-11086-10	Sequence 10, Appl
21	33.4	3.3	299	US-09-539-331D-20130	Sequence 20130, A
22	33.4	3.3	497	US-09-785-276A-60792	Sequence 60792, A
23	33.4	3.3	1292	US-09-634-754C-493	Sequence 493, App
24	33.4	3.3	1292	US-09-634-754D-493	Sequence 493, App
25	33.4	3.3	2324	US-09-629-469A-14737	Sequence 14737, A

26	33.2	3.3	168575	US-10-178-194-1	Sequence 1, Appl
27	33	3.3	495	US-09-620-393B-1200	Sequence 1200, Ap
28	33	3.3	495	US-09-935-625-6643	Sequence 6643, Ap
29	33	3.3	495	US-09-935-625-18919	Sequence 18919, A
30	33	3.3	567	US-10-027-632-43342	Sequence 43342, A
31	33	3.3	567	US-10-027-632-43343	Sequence 43343, A
32	33	3.3	567	US-10-027-632-66444	Sequence 66444, A
33	33	3.3	567	US-10-027-632-66445	Sequence 66445, A
34	33	3.3	567	US-10-027-632-311165	Sequence 311165, A
35	33	3.3	567	US-10-027-632-311166	Sequence 311166, A
36	33	3.3	854	US-10-027-632-151631	Sequence 151631, A
37	33	3.3	992	US-10-144-860-111	Sequence 112, App
38	33	3.3	2497	US-09-705-256A-112	Sequence 112, App
39	32.8	3.3	166	US-10-113-872-1580	Sequence 1580, Ap
40	32.8	3.3	517	US-10-027-632-281359	Sequence 281359, Ap
41	32.8	3.3	1859	US-09-705-256A-6386	Sequence 6386, Ap
42	32.8	3.3	4649	US-09-919-002-1530	Sequence 1530, Ap
43	32.8	3.3	13578	US-10-105-299-11948	Sequence 11948, A
44	32.6	3.3	459	US-10-098-754-659	Sequence 659, App
45	32.6	3.3	507	US-10-027-632-194618	Sequence 194618, A

ALIGNMENTS

```
RESULT 1
US-09-811-352B-1
; Sequence 1, Application US/09811352B
; GENERAL INFORMATION:
; APPLICANT: Jonsdottir, Solveig
; APPLICANT: Jonsdottir, Stf
; APPLICANT: Reynisdottir, Stigdur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-000
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1191139
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-811-352B-1

Query Match      3.7%; Score 37.4; DB 5; Length 1191139;
Best Local Similarity 52.2%; Pred. No. 63;
Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 390 ttttttaatggaagcaaggttgcaaacacatgcatltaaacacaggaataat 449
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287753 ttatgattactagcacacaggactattttatctaactatcttaacataacaaat 287812

QY 450 tccaacacccatgacatctcaaacacatgcacacgacgacgacgacgagtg 509
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287813 tgaataattcttggaatcatcatccacttaataatggaagtaacatttggaanaa 287872

QY 510 aacgaagaactgaataatcaacatccacagtgctgagtc 548
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287873 atataacatgaaatcgcacccagctgaagaaatc 287911

RESULT 2
US-10-140-924-1
; Sequence 1, Application US/10140924
; GENERAL INFORMATION:
; APPLICANT: Grelarsdottir, Solveig
; APPLICANT: Jonsdottir, Stf
; APPLICANT: Reynisdottir, Stigdur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-000
; CURRENT FILING DATE: 2002-05-07
```

```
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FASTSEQ for Windows version 4.0
; SEQ ID NO 1
; LENGTH: 1191139
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-924-1
```

```
Query Match          3.7%; Score 37.4; DB 7; Length 1191139;
Best Local Similarity 52.2%; Pred. No. 63;
Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
```

```
OY 390 tttttttaaaggaagagttggcaaacatgcatctttcaacaagaataat 449
    || || || || || || || || || || || || || || || || || ||
DB 287753 ttatgattactgcaacagggactattttatccaactctttacataaataat 287812

OY 450 tctcaaacccatgacatgcaatctcacaaccatgacggaggtcagtcgag 509
    || || || || || || || || || || || || || || || || || ||
DB 287813 tgtaaatttctaggaattcattccacttaaaataggaagtacatttggaaaaa 287872

OY 510 aacgaagactgaaatcaacatcccatgtgtcgagtc 548
    || || || || || || || || || || || || || || || || || ||
DB 287873 atattaacataagaaatcagcatcccggttaagaatc 287911
```

```
RESULT 3
US-10-067-514-1
; Sequence 1, Application US/10067514
; GENERAL INFORMATION:
; APPLICANT: GretaSodttr, Solveig
; APPLICANT: Jonsdottir, Sif
; APPLICANT: Reyaisdottir, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-003
; CURRENT APPLICATION NUMBER: US/10/067,514
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 09/811/352
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691139
; TYPE: DNA
; ORGANISM: Human
US-10-067-514-1
```

```
Query Match          3.7%; Score 37.4; DB 7; Length 1691139;
Best Local Similarity 52.2%; Pred. No. 71;
Matches 83; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
```

```
OY 390 tttttttaaaggaagagttggcaaacatgcatctttcaacaagaataat 449
    || || || || || || || || || || || || || || || || || ||
DB 787752 ttatgattactgcaacagggactattttatccaactctttacataaataat 787811

OY 450 tctcaaacccatgacatgcaatctcacaaccatgacggaggtcagtcgag 509
    || || || || || || || || || || || || || || || || || ||
DB 787812 tgtaaatttctaggaattcattccacttaaaataggaagtacatttggaaaaa 787871

OY 510 aacgaagactgaaatcaacatcccatgtgtcgagtc 548
    || || || || || || || || || || || || || || || || || ||
DB 787872 atattaacataagaaatcagcatcccggttaagaatc 787910
```

```
RESULT 4
PCT-US02-25766-10980/c
; Sequence 10980, Application PC/TUS0225766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MUNGER, William E
; APPLICANT: PAULI, Ronald
; APPLICANT: SUN, Hongwei
```

```
; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-NO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/311,837
; NUMBER OF SEQ ID NOS: 13946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10980
; LENGTH: 6493
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X98534
; NAME/KEY: misc_feature
; LOCATION: (1)..(6493)
; OTHER INFORMATION: n = a or c or g or t
PCT-US02-25766-10980
```

```
Query Match          3.7%; Score 37.2; DB 1; Length 6493;
Best Local Similarity 52.6%; Pred. No. 9.4;
Matches 81; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
```

```
OY 598 catgacaatacataagtcataaccctacaattgttttggagcagagtggtgctt 657
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DB 3453 CAAGTCCAAAGTATTTTGGGGCCCAAGTATTTTGGTTTGGTTGTGTGTGT 3394

OY 658 ttttttacaagaatgcatagctggcccgcatgctgctgagatcgatcgatcgctg 717
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DB 3393 TTGTTTGAAGACAGTCACATTCTATTTCACAGCTGGAGTGCAGGCAGATGATGGCTCG 3334

OY 718 gagacgaggaatcagacactcaccactgct 751
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DB 3333 CTGAGGCTCAACTCTCGGCTCAAGTATTCCT 3300
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RESULT 5
US-10-155-881-25269/c
; Sequence 25269, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 25269
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-155-881-25269
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Query Match          3.6%; Score 35.6; DB 7; Length 691;
Best Local Similarity 54.6%; Pred. No. 11;
Matches 71; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
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    || || || || || || || || || || || || || || || || || ||
DB 173 CCGTGCATGTGGCCCTCTCGCGCAGCTGTGAGCAGGGCGGCTGCTCGCGCGCC 114

OY 888 gtgcctccacgctgcgtgcgtgcacactgtgctgctgcgcgcgcaggaaggagga 947
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; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 600
; LENGTH: 10495
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-600
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Best Local Similarity 53.8%; Pred. No. 71;
Matches 71; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
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QY 647 ggttggtcttcttttttcaacgaatgcatagctggcccgatgctgagatcgg 706
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DB 2416 CTTTGGACTTTTGTGTCATTTTCACATGTTCTTCTGGCAGCATTAACAGAACTCAG 2357
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QY 707 atgatggtcgg 718
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DB 2356 CTTCTCGGCGCTG 2345
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RESULT 13

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; Sequence 482, Application PC/TUS0209105
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS951PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09105
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; NUMBER OF SEQ ID NOS: 779
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 482
; LENGTH: 15932
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-09105-482
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Query Match 3.4%; Score 34.4; DB 1; Length 15932;
Best Local Similarity 57.4%; Pred. No. 84;
Matches 62; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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QY 546 gtgcgaagaagatgacatgaagatgcgtattacattcattacatgtaca 605
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DB 3900 ggttaaaaaaacaagaacatgtatcatgtataatgtatccatttataata 3959
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QY 606 aatacataatgtacacctacaattgtttttgagcagagtggtg 653
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DB 3960 cacacataaagagactgttaagaacttgggagcgagcgagtg 4007
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RESULT 14
PCT-US02-09370-1049
; Sequence 1049, Application PC/TUS0209370
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
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; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS954PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09370
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; NUMBER OF SEQ ID NOS: 1834
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Homo sapiens
PCT-US02-09370-1049
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Best Local Similarity 57.4%; Pred. No. 84;
Matches 62; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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DB 3960 cacacataaagagactgttaagaacttgggagcgagcgagtg 4007
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RESULT 15

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US-10-105-299-6415
; Sequence 6415, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6415
; LENGTH: 15932
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-6415
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Best Local Similarity 57.4%; Pred. No. 84;
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1001	100.0	11463	19	US-09-508-377-10	Sequence 10, Appl
2	141.2	14.1	104364	20	US-09-534-859-337	Sequence 337, App
3	141.2	14.1	104364	31	US-09-803-736-337	Sequence 337, App
4	133	13.3	416	23	US-09-606-977-62778	Sequence 62778, A
5	131.6	13.1	102897	31	US-09-803-736-1401	Sequence 1401, Ap
6	128.2	12.8	2853	11	US-08-726-705-3	Sequence 3, Appl
7	128.2	12.8	2853	23	US-09-609-040-3	Sequence 42943, A
8	127.8	12.8	2368	24	US-09-620-392-42943	Sequence 20657, A
9	127.8	12.8	2368	28	US-09-702-134-20657	Sequence 91233, A
10	127.8	12.8	2368	31	US-09-815-264-91233	Sequence 26244, A
11	126.6	12.6	400	22	US-09-572-409-26244	Sequence 16419, A
12	123.6	12.3	345	31	US-09-804-730-16419	Sequence 14485, A
13	123.6	12.3	345	17	US-09-189-657-14485	Sequence 98960, A
14	111.6	11.1	23449	17	US-09-330-889A-2	Sequence 2, Appl
15	109	10.9	2655	33	US-09-887-272A-4612	Sequence 4612, Ap
16	109	10.9	3017	25	US-09-654-617-385160	Sequence 385160, A
17	109	10.9	3017	27	US-09-684-016-385160	Sequence 385160, A
18	105.8	10.6	724	33	US-09-865-439A-54797	Sequence 54797, A
19	105.8	10.6	724	59	US-09-207-458-98860	Sequence 98860, A
20	105.8	10.6	2446	29	US-09-731-166-9	Sequence 9, Appl
21	105.4	10.5	2559	30	US-09-792-127-1	Sequence 1, Appl
22	105.4	10.5	3039	30	US-09-620-392-13950	Sequence 13950, A
23	103.2	10.3	21414	24	US-09-702-134-28820	Sequence 28820, A
24	103.2	10.3	21414	28	US-09-815-264-77542	Sequence 77542, A
25	103.2	10.3	21414	31	US-09-325-448-1027	Sequence 1027, Ap
26	102.4	10.2	1642	71	US-09-850-147-1243	Sequence 1243, Ap
27	101.8	10.2	378	32	US-09-202-213-1240	Sequence 1240, Ap
28	101.8	10.2	384	25	US-09-654-617-454409	Sequence 454409, A
29	101.8	10.2	384	27	US-09-684-016-454409	Sequence 454409, A
30	101.8	10.2	384	27	US-09-692-257A-1612	Sequence 1612, Ap
31	101.4	10.1	388	27		

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32 101.4 10.1 388 55 US-60-162-747-1455 Sequence 1455, Ap
33 100.8 10.1 686 33 US-09-865-439A-53497 Sequence 53497, A
34 100.8 10.1 686 33 US-60-207-458-97660 Sequence 97660, A
35 100.8 10.1 2087 14 US-09-091-052-9 Sequence 9, Appli
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ALIGNMENTS

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RESULT 1
US-09-508-377-10
; Sequence 10, Application US/09508377
; GENERAL INFORMATION:
; APPLICANT: KALEEN, ZHONGYILI
; APPLICANT: MORELL, MATTHEW
; APPLICANT: RAHMAN, SADEOUR
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 054270/0126
; CURRENT APPLICATION NUMBER: US/09/508, 377
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: AU PP 2509
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/AU98/00743
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: AU PP 9108
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11463
; TYPE: DNA
; ORGANISM: Triticum tauschii
US-09-508-377-10
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Best Local Similarity 100.0%; Pred. No. 7.8e-231;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 5400 cccatcctaattgagcagggccctatcgccgaatatttccatctataatgtgcta 5459
QY 961 cgtgactcttcttctcagatgatttaaccaggttgaca 1001
DB 5460 cgtgactcttcttctcagatgatttaaccaggttgaca 5500
```

```
RESULT 2
US-09-534-859-337
; Sequence 337, Application US/09534859
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Last, Robert L.
; APPLICANT: Levin, Irena M.
; APPLICANT: Norris, Susan R.
; APPLICANT: Parnell, Steven D.
; APPLICANT: Rounsley, Roger C.
; TITLE OF INVENTION: PLANT POLYMORPHIC MARKERS AND USES THEREOF
; FILE REFERENCE: 38-10(15493)B
; CURRENT APPLICATION NUMBER: US/09/534, 859
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 1127
; SEQ ID NO 337
; LENGTH: 104364
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-534-859-337
```

```
Query Match 14.1%; Score 141.2; DB 20; Length 104364;
Best Local Similarity 62.2%; Pred. No. 9.3e-23;
Matches 270; Conservative 0; Mismatches 138; Indels 26; Gaps 2;
```

```
QY 313 caggaaccgaataattcatatgcttaattttagagtgaggtgttgccaagaattaa 372
```

Db	16557	caggacacaaagataataacatatgccaatttgagatgatatgtactcccggtataaa	16616
Qy	373	aggcttggatacaatgycagtgccagataatggcaalccgcggagcaltcatatgcaagc	432
Db	16617	aagctagcgtataatgctgctgagataatgccaatccaagcagcatgctactatgccaagc	16676
Qy	433	tttggtgtatcaacacaaatccattttttctgtataactcttaccocatttgagcttt	492
Db	16677	tttgggtat-----cttcctcttcagataataacatgctaccactatccattt	16726
Qy	493	aacatccatgcttcacatgacacataaatttggataataacccttatagatatatgt	552
Db	16727	aatgaatacctgctttaaaagccattgttggatcttcagagtc-----gt	16770
Qy	553	acaatacaactagatattcttgaanaagataatttatgttggctgttgcaggtac	612
Db	16771	aaaacctattgtctccctcttgatgaatgagcatgcatgtacttgcataatgcacaggtat	16830
Qy	613	catgttactaaattttttgcaccaaagtcgcgcttttggaaactccagagagacttaaatcc	672
Db	16831	catgtagacaatttttttcgcacctgacgcgcgcttttggaaacctgcagacttaaatcc	16890
Qy	673	ttgatcgaatagacacatgagccttgggttgcgttgccttcatgabatgtttcataggtaa	732
Db	16891	ttgatagacaagaagctcatgagctagtcctgtgttgcctgatgatatatgtgcacaggtat	16950
Qy	733	ttgatgcatttaa	746
Db	16951	tggtctctctttaa	16964

```

RESULT      3
US-09-803-736-337
: Sequence 337, Application US/09803736
: GENERAL INFORMATION:
: APPLICANT: Bush, David F.
: APPLICANT: Levin, Irena M.
: APPLICANT: Norris, Susan R.
: APPLICANT: Rounsley, Steven D.
: APPLICANT: Miegand, Roger C.
: TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
: FILE REFERENCE: 38-10415493D
: CURRENT APPLICATION NUMBER: US/09/803,736
: CURRENT FILING DATE: 2001-03-12
: PRIOR APPLICATION NUMBER: US 09/534,859
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
: PRIOR FILING DATE: 2000-10-20
: NUMBER OF SEQ ID NOS: 1582
: SEQ ID NO 337
: LENGTH: 104364
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: US-09-803-736-337

```

Query Match	14.1%;	Score 141.2;	DB 31;	Length 104364;
Best Local Similarity	62.2%;	Pred. No. 9.3e-23;		
Matches 270;	Conservative	0;	Mismatches 138;	Indels 26; Gaps 2

Oy	313	caggaacccgaagataaaattcatabgcactatlttagggatgagggttttgccaagaattaa	372
Db	16557	caggacaaccaagaataaacatcacatgcccaactttagagatgatgtactctcccgtataaa	16616
Oy	373	agaccttgatatacaatgcacgtgcaggtaatgycgaatcccgagcatctcatcatactcaagc	432
Db	16617	aagcctcaggtctaatacgtcgttcgaagataatgycatccatcaagagcatgcctactatgcagc	16676
Oy	433	ttagtgtattcaacaacccaatttttctcgtatatacactcttcaccocatitggagctatt	492
Db	16677	tttggattt-----cttcctcttcagataataacatctctaccctaccatcaatt	16736

[illegible]

```

RESULT      4
US-09-606-977-62778
; Sequence 62778, Application US/09606977
; GENERAL INFORMATION:
; APPLICANT:      Byrum, Joseph R.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15877)B
; CURRENT APPLICATION NUMBER: US/09/606,977
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 82359
; SEQ ID NO 62778
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: unsure at all n locations
US-09-606-977-62778

```

Query Match	13.38;	Score 133;	DB 23;	length 416;
Best Local Similarity	66.38;	Pred. No. 1.4e-21;		
Matches 240;	Conservative	0;	Mismatches 105;	Indels 17; Gaps 3;

QY	387	tgcagtcagataatgycgaatccaggagcatlctactatgacaaagcttgggtattaca	446
DB	1	tgcagtcagataatgycgaatccagacatcttatattcaagagtttgggtattaca	60
QY	447	ca-----atccatttttttcgtataaac-----ttcacccatttggagctaa	490
DB	61	ctttcaatgcatccatccatcttcttgggtttctgttttttccatccatctgaaatc	120
QY	491	ttacatctctaattgcttctacgacata-aatatctgataataaccttattagataat	549
DB	121	tgtccttctaattgcttctgacaaacaggagacatctgacatcgccatctaattttcagg	180
QY	550	agtacactacactagratctctgtaaaagaatccatttatgtgtgtgcttgcagg	609
DB	181	ccataataacatcatatgatttcttacttttatacgtgatttcgtataattccatnttcagg	240
QY	610	taccatgttactaattttttgcaccaggatgcgcttttgtaactccaggagacttaaa	669
DB	241	taccatgttactgaatttttttgcgcccaagtgcgcttttggagatccaggagacttaaa	300
QY	670	tccctgatacgaatagacacatgagcttggtttgcctgttcttaacgataatgtttcatagg	729
DB	301	tcccttattgtataaagcgcatgagcttggctgtgtatgcttatgataatgtttcatagg	360
QY	730	ta 731	
DB	361	ta 362	


```
APPLICANT: Willmitzer, et al.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE
FILE REFERENCE: 514413-3515.1
CURRENT APPLICATION NUMBER: US/09/609,040
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: PCT/EP92/00302
PRIOR FILING DATE: 1992-02-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 2853
TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: CDS
LOCATION: (313)..(2499)
OTHER INFORMATION: BRANCHING ENZYME
US-09-609-040-3
```

```
Query Match 12.8%; Score 128.2; DB 23; Length 2853;
Best Local Similarity 91.3%; Pred. No. 3.8e-20;
Matches 136; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 313 caggaaacggaagataatcatatgctaattttagggatgagtggttgcgaagaattaa 372
DB 997 ccggagaccggaagataatcatatgctaattttagggatgagtggttgcgaagaattaa 1056
QY 373 aggccttgatatacatgcatgcatgaataatgcaatccaggaacatcatatgaagc 432
DB 1057 aggccttgatatacatgcatgcatgaataatgcaatccaggaacatcatatgaagc 1116
QY 433 ttgggtattcacacaatccatttttc 461
DB 1117 ttgggtattcacatgcttactaatttttgc 1145
```

```
RESULT 8
US-09-620-392-42943/C
Sequence 42943, Application US/09620392
GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey A.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
APPLICANT: McIninch, James
TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
FILE REFERENCE: 38-21(51237)E
CURRENT APPLICATION NUMBER: US/09/620,392
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 69652
SEQ ID NO 42943
LENGTH: 2368
TYPE: DNA
ORGANISM: Oryza sativa
US-09-620-392-42943
```

```
Query Match 12.8%; Score 127.8; DB 24; Length 2368;
Best Local Similarity 75.4%; Pred. No. 4.5e-20;
Matches 159; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
```

```
QY 548 atagaaacactacactagtagtctcgaaagatactattatgttggtgctgttcca 607
DB 2315 atagaaacactacactagtagtctcgaaagatactattatgttggtgctgttcca 2256
QY 608 gtatcacttactaattttttgacaagaagccgttttggaactccagaagacttaa 667
DB 2255 ggtatcacttactaattttttgacaagaagccgttttggaactccagaagacttaa 2196
QY 668 aatccttgatcgatagagacatgagctgtgttgctgttcttatgatattgttcata 727
DB 2195 aatccttgatcgatagagacatgagctgtgttgctgttcttatgatattgttcata 2136
```

```
QY 728 ggtaatagccaatttaatttagctgttt 758
DB 2135 ggtaatagccaatttaatttagctgttt 2105
```

```
RESULT 9
US-09-702-134-20657/C
Sequence 20657, Application US/09702134
GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey A.
APPLICANT: Cao, Yongwei
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
APPLICANT: McIninch, James
APPLICANT: Wu, Wei
TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
FILE REFERENCE: 38-21(51237)E
CURRENT APPLICATION NUMBER: US/09/702,134
CURRENT FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 52202
SEQ ID NO 20657
LENGTH: 2368
TYPE: DNA
ORGANISM: Oryza sativa
US-09-702-134-20657
```

```
Query Match 12.8%; Score 127.8; DB 28; Length 2368;
Best Local Similarity 75.4%; Pred. No. 4.5e-20;
Matches 159; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
```

```
QY 548 atagaaacactacactagtagtctcgaaagatactattatgttggtgctgttcca 607
DB 2315 atagaaacactacactagtagtctcgaaagatactattatgttggtgctgttcca 2256
QY 608 gtatcacttactaattttttgacaagaagccgttttggaactccagaagacttaa 667
DB 2255 ggtatcacttactaattttttgacaagaagccgttttggaactccagaagacttaa 2196
QY 668 aatccttgatcgatagagacatgagctgtgttgctgttcttatgatattgttcata 727
DB 2195 aatccttgatcgatagagacatgagctgtgttgctgttcttatgatattgttcata 2136
QY 728 ggtaatagccaatttaatttagctgttt 758
DB 2135 ggtaatagccaatttaatttagctgttt 2105
```

```
RESULT 10
US-09-815-264-91233/C
Sequence 91233, Application US/09815264
GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey A.
APPLICANT: Cao, Yongwei
APPLICANT: Dotson, Stanton B.
APPLICANT: Koshi, Jeffrey M.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
APPLICANT: McIninch, James
APPLICANT: Wu, Wei
TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 91233
LENGTH: 2368
TYPE: DNA
```



```
QY 316 gaaccgaataattcatatgcttaatttagagatgaggtgtgtgccaaagaattaaag 375
      |||||||
Db 45 gaaccgaataattcatatgcttaatttagagatgaggtgtgtgccaaagaattaaag 104
QY 376 ctgtgataaatgcatgtagataatggaatcagagacatcactacatacgaactt 435
      |||||||
Db 105 ctgtgataaatgcatgtagataatggaatcagagacatcactacatacgaactt 164
QY 436 gggatcacaacatccatttttc 461
      |||||
Db 165 gggatcacaatcatttttttc 190
```

RESULT 14

```
US-09-330-889A-2
; Sequence 2, Application US/09330889A
; GENERAL INFORMATION:
; APPLICANT: Gultinan, Mark A.
; APPLICANT: Kim, Kyung-Nam
; TITLE OF INVENTION: Expression Control Elements from Genes
; FILE REFERENCE: Penn State 1465
; CURRENT APPLICATION NUMBER: US/09/330,889A
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: US 60/089,049
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/089,050
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 23449
; TYPE: DNA
; ORGANISM: Zea mays
US-09-330-889A-2
```

```
Query Match 11.1%; Score 111.6; DB 17; Length 23449;
Best Local Similarity 81.6%; Pred. No. 7.9e-16;
Matches 129; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
```

```
QY 309 ttgacaggaacggaataattcatatgcttaatttagagatgaggtgtgtgccaaagt 368
      |||||||
Db 7585 tgatttgagacggaataataacacataatgtaactttagagatgaggtgtgtgccaaagt 7644
QY 369 taaaggttgatgataatgcatgtagataatggaatcagagacatcactacatacgc 428
      |||||
Db 7645 aaaaacttgatgataatgcatgtagataatggaatcagagacatcactacatacgc 7704
QY 429 aagcttggtatcacaatccattttttctgtat 466
      |||||||
Db 7705 aagcttggtatcacaatccattttttctgtat 7742
```

RESULT 15

```
US-09-887-272A-4612
; Sequence 4612, Application US/09887272A
; GENERAL INFORMATION:
; APPLICANT: Hou, Yu-Ming
; APPLICANT: Quan, Sheng
; APPLICANT: Chang, Hur-Song
; APPLICANT: Zhu, Tong
; APPLICANT: Whitlam, Steve
; APPLICANT: Goff, Steve
; APPLICANT: Glazebrook, Jane
; APPLICANT: Chen, Wenguihong
; APPLICANT: Katagiri, Fumiki
; APPLICANT: Xie, Zhiyi
; APPLICANT: Tao, Yi
; APPLICANT: Zou, Guangzhou
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: PLANT GENES INVOLVED IN DEFENSE AGAINST
```

```
; TITLE OF INVENTION: PATHOGENS
; FILE REFERENCE: 1360.003US2
; CURRENT APPLICATION NUMBER: US/09/887,272A
; CURRENT FILING DATE: 2001-06-23
; PRIOR APPLICATION NUMBER: 60/213,634
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/214,926
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/261,320
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/264,353
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/273,879
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 09/887,271
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 6813
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4612
; LENGTH: 2655
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-887-272A-4612
```

```
Query Match 10.9%; Score 109; DB 33; Length 2655;
Best Local Similarity 83.2%; Pred. No. 1.6e-15;
Matches 124; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
```

```
QY 313 caagaacggaataattcatatgcttaatttagagatgaggtgtgtgccaaagaattaa 372
      |||||||
Db 1093 ccgaacggaataataacacataatgtaatttagagatgaggtgtgtgccaaagaattaa 1152
QY 373 aagcttgatgataatgcatgtagataatggaatcagagacatcactacatacgaagc 432
      |||||||
Db 1153 aagcttgatgataatgcatgtagataatggaatcagagacatcactacatacgaagc 1212
QY 433 ttgggtatcacaatccatttttc 461
      |||||||
Db 1213 ttgggtatcacaatccatttttc 1241
```

Search completed: September 12, 2002, 10:11:16
Job time: 9624 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 10:11:16 : Search time 5258.2 Seconds
(without alignments)
4118.621 Million cell updates/sec

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Perfect score: 1001
Sequence: 1 tccgacatagacacatgta.....ctgagacatagctttttg 1001

Scoring table:
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Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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71: /cgn2_6/ptodata/1/pna/US05086.COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US05086.COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US05086.COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US05086.COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US05086.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	11463	19 US-09-508-377-10	Sequence 10, Appl
2	223.2	22.3	23449	14 US-09-330-889A-2	Sequence 13, Appl
3	187.2	18.7	21414	24 US-09-620-352-13950	Sequence 28820, A
4	187.2	18.7	21414	31 US-09-702-134-28820	Sequence 77542, A
5	187.2	18.7	21414	38 US-09-815-264-77542	Sequence 3410, Ap
6	136.4	13.6	1119	71 US-60-325-448-3410	Sequence 3, Appl
7	134.8	13.5	2853	11 US-08-726-705-3	Sequence 4612, Ap
8	128.8	12.9	2655	33 US-09-887-212A-4612	Sequence 91564, A
9	122	12.2	420	17 US-09-304-517A-91564	Sequence 21714, A
10	122	12.2	420	36 US-09-985-678-91564	Sequence 91564, A
11	122	12.2	421	17 US-09-394-745-21714	Sequence 42955, A
12	122	12.2	421	22 US-09-565-306-42955	Sequence 91564, A
13	122	12.2	499	17 US-09-371-146A-91564	Sequence 2236, Ap
14	122	12.2	531	32 US-09-845-526A-2236	Sequence 2236, Ap
15	122	12.2	531	29 US-60-202-214-2236	Sequence 1807, Ap
16	122	12.2	2446	59 US-09-731-166-9	Sequence 9, Appl
17	120.4	12.0	399	24 US-09-637-086A-1807	Sequence 1807, Ap
18	120.4	12.0	399	24 US-09-637-086A-1807	Sequence 204100, Ap
19	120.4	12.0	399	24 US-09-654-617-204100	Sequence 204100, Ap
20	120.4	12.0	399	25 US-09-654-617-204100	Sequence 204100, Ap
21	120.4	12.0	399	25 US-09-654-617-204100	Sequence 204100, Ap
22	120.4	12.0	441	17 US-09-684-016-204100	Sequence 204100, Ap
23	120.4	12.0	441	17 US-09-394-745-21048	Sequence 33904, A
24	120.4	12.0	441	22 US-09-565-306-39904	Sequence 33904, A
25	120.4	12.0	441	36 US-09-985-678-93092	Sequence 93092, A
26	120.4	12.0	527	17 US-09-371-146A-93092	Sequence 93092, A
27	118.8	11.9	3017	25 US-09-654-617-385160	Sequence 385160, A
28	118.8	11.9	3017	27 US-09-684-016-385160	Sequence 48567, A
29	117.8	11.8	413	22 US-09-394-745-48567	Sequence 69979, A
30	117.8	11.8	413	22 US-09-565-306-69979	Sequence 2386, Ap
31	117.8	11.8	567	32 US-09-845-526A-2386	

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32 117.8 11.8 567 59 US-60-202-214-2386 Sequence 2386, Ap
33 117.2 11.7 366 32 US-09-850-147-7191 Sequence 7191, Ap
34 117.2 11.7 366 59 US-60-202-213-7178 Sequence 7178, Ap
35 117.2 11.7 368 32 US-09-850-147-4345 Sequence 4345, Ap
36 117.2 11.7 368 59 US-60-202-213-4342 Sequence 4342, Ap
37 117.2 11.7 725 25 US-09-654-617-452844 Sequence 452844,
38 117.2 11.7 725 27 US-09-684-016-452844 Sequence 452844,
39 115.8 11.6 444 26 US-09-667-188A-2250 Sequence 2250, Ap
40 115.8 11.6 444 54 US-60-155-006-3134 Sequence 3134, Ap
41 115.8 11.6 457 26 US-09-667-188A-1619 Sequence 1619, Ap
42 115.8 11.6 457 54 US-60-155-006-2503 Sequence 2503, Ap
43 115.6 11.5 365 32 US-09-850-147-6476 Sequence 6476, Ap
44 115.6 11.5 365 59 US-60-202-213-6463 Sequence 6463, Ap
45 110.8 11.1 291 17 US-09-304-517A-49291 Sequence 49291, A
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ALIGNMENTS

```
RESULT 1
US-09-508-377-10
: Sequence 10, Application US/09508377
: GENERAL INFORMATION:
: APPLICANT: KALEEN, ZHONGYILI
: APPLICANT: MORELL, MATTHEW
: APPLICANT: RAHMAN, SADEOUR
: TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS
: FILE REFERENCE: 054270/0126
: CURRENT APPLICATION NUMBER: US/09/508, 377
: CURRENT FILING DATE: 2000-06-09
: PRIOR APPLICATION NUMBER: AU PP 2509
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: PCT/AU98/00743
: PRIOR FILING DATE: 1998-09-11
: PRIOR APPLICATION NUMBER: AU PP 9108
: PRIOR FILING DATE: 1997-09-12
: NUMBER OF SEQ ID NOS: 71
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 10
: LENGTH: 11463
: TYPE: DNA
: ORGANISM: Triticum tauschii
US-09-508-377-10
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Query Match 100.0%; Score 1001; DB 19; Length 11463;
Best Local Similarity 100.0%; Pred. No. 3.2e-231;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 tcgcacatagacagcatgacacatatacagctctctctgtgcagagatagtattca 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9500 tcgcacatagacagcatgacacatatacagctctctctgtgcagagatagtattca 9559

QY 61 tggctctgagatagcttaactcttcgcatgacgctgtgcatacacaataatgat 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9560 tggctctgagatagcttaactcttcgcatgacgctgtgcatacacaataatgat 9619

QY 121 cagccttccacatgggttaggtgtggaaggtcattcaattcattcaggaatgaatt 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9620 cagccttccacatgggttaggtgtggaaggtcattcaattcattcaggaatgaatt 9679

QY 181 tgggcattctgtcagcttattacacattatgcatcttcgcatgattgttgaattca 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9680 tgggcattctgtcagcttattacacattatgcatcttcgcatgattgttgaattca 9739

QY 241 attgaacattgtcttcttccacattgtatgtattatgtatctgttgcctccaagag 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9740 attgaacattgtcttcttccacattgtatgtattatgtatctgttgcctccaagag 9799

QY 301 gaattactcttattacttggaagatgagatatttccagaagcccaaacctct 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9800 gaattactcttattacttggaagatgagatatttccagaagcccaaacctct 9859
```

```
QY 361 tccaaccgcaaatctcccttggaaataacaatagtattgataaagccgcgtagat 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9680 tccaaccgcaaatctcccttggaaataacaatagtattgataaagccgcgtagat 9919

QY 421 ttgattctgtaagtttaagctgtgtctattacattccctactaattatttggccatt 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9920 ttgattctgtaagtttaagctgtgtctattacattccctactaattatttggccatt 9979

QY 481 tattcttgtaaatcaataatgtttttagaagaatcaacattgctttgtatgtttg 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9980 tattcttgtaaatcaataatgtttttagaagaatcaacattgctttgtatgtttg 10039

QY 541 tagacgttaacaataagatgtgtttagaagttgttgcatttaaaatacatgatttt 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10040 tagacgttaacaataagatgtgtttagaagttgttgcatttaaaatacatgatttt 10099

QY 601 gcaaggagatgcaattttcttaagatacgtgtatgcaagatgcatgcaagatgca 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10100 gcaaggagatgcaattttcttaagatacgtgtatgcaagatgcatgcaagatgca 10159

QY 661 gcatcttgaggaataataggggtatgcatgctgtgttcttcttgcataaagctcac 720
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10160 gcatcttgaggaataataggggtatgcatgctgtgttcttcttgcataaagctcac 10219

QY 721 agtttaacgtcagctctcttcaagtgttaaaaaaagtgtaaatattcctgtaatga 780
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10220 agtttaacgtcagctctcttcaagtgttaaaaaaagtgtaaatattcctgtaatga 10279

QY 781 tgaaaactgtcacaagcgagctggaattgtcttccacaaacttttcttaagtgc 840
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10280 tgaaaactgtcacaagcgagctggaattgtcttccacaaacttttcttaagtgc 10339

QY 841 ttgtgtattgatacatatacagcactgcaaatgttaactgagttatgacatctgagca 900
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10340 ttgtgtattgatacatatacagcactgcaaatgttaactgagttatgacatctgagca 10399

QY 901 ccagatatttccacggaacatgaggaagatgaagtgatcatcctcctcaaaagagatatt 960
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10400 ccagatatttccacggaacatgaggaagatgaagtgatcatcctcctcaaaagagatatt 10459

QY 961 ggtattgttttcaactccactgagcaatagctttttg 1001
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10460 ggtattgttttcaactccactgagcaatagctttttg 10500
```

```
RESULT 2
US-09-330-889A-2
: Sequence 2, Application US/09330889A
: GENERAL INFORMATION:
: APPLICANT: Guiltinan, Mark A.
: APPLICANT: Kim, Kyung-Nam
: TITLE OF INVENTION: Expression Control Elements from Genes
: TITLE OF INVENTION: Encoding Starch Branching Enzymes
: FILE REFERENCE: Penn State 1465
: CURRENT APPLICATION NUMBER: US/09/330, 889A
: CURRENT FILING DATE: 1999-06-11
: PRIOR APPLICATION NUMBER: US 60/089, 049
: PRIOR FILING DATE: 1998-06-12
: PRIOR APPLICATION NUMBER: US 60/089, 050
: PRIOR FILING DATE: 1998-06-12
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 23449
: TYPE: DNA
: ORGANISM: Zea mays
US-09-330-889A-2
```

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Query Match 22.3%; Score 223.2; DB 17; Length 23449;
Best Local Similarity 58.6%; Pred. No. 6.3e-43;
Matches 649; Conservative 0; Mismatches 333; Indels 126; Gaps 10;
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:
:
: CURRENT APPLICATION NUMBER: US/09/702,134
:
: CURRENT FILING DATE: 2000-10-31
:
: NUMBER OF SEQ ID NOS: 52202
:
: SEQ ID NO 28820
:
: LENGTH: 21414
:
: TYPE: DNA
:
: ORGANISM: Oryza sativa
:
: US-09-702-134-28820

```

Query Match	18.7%;	Score 187.2;	DB 28;	Length 21414;
Best Local Similarity	-71.5%;	Pred. No. 3.1e-34;		
Matches 306;	Conservative	0;	Mismatches 108;	Indels 14;
				Gaps 4;

QY	19	gaacatcaaaagctctcttgcgcagatbtaagattcaatgcgtctgcgaataagct-	77
Db	10778	GAACCTCACATCTCTACTTATGACGAGATGATGATTTATGGCTCTGACACACCGG	107129
QY	78	caactcttcgcattgattcgtgcataagattacataaaatgatcagcgtctgtccacatg	137
Db	10718	CACCTCTTACGATTCATGCTGGAAATAGCATTCGATTTAAATGATTAGACTTATTCACCAATGG	106599

Qy 138 gttcaagtgtgtaagcgtatcttaactcatcggaatagatglttggccatccgtgcagt 197
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 10658 GGTTAGGAGAGAAGCCTATCTTAACCTTATGGGAATGACTTCGACATCCTGGTGAGA 10599

OY 198 cttacaacattatctgcatctcgtgatgttactgt-----atttgaa 248
||| ||| | ||| ||| |||
Db 10538 tttaataacatcacacaccagtgttgcctaatttatcaaccttcgaattgatga 10539
||||| ||| ||| ||| |||

Oy 249 cagctttcttcaacatgttatgtatatgtaatcgttgctccaaaggagaagttaa 308
|| || || || || || || || || || || || || || || || || || || || ||
Db 10538 CAATGGTCTTGTCACCTAGATTTTCTCGGGAACAATTGGCT---AAAGGCATTGAT 10482

OY 309 cttctattacttgcgaatygatatagatttcagaaggcccaacaactccticcaaccg 368
 || | ||| | ||||| | ||||| | ||||| | ||||| |
Db 10481 CTACCTTTTATTTTTGCAGATTGATTTTCACAGAGCCTCCACAAGTACTTCCAATG 10422

OY 369 gcaaaagtctccccctggaataacaatagttatgataaaygcgcggtagattgatctt 428
| | | | |
Db 10421 GTAAATTCATCCACGGAATACAACAGTTATGTAAATGCCGTCAAGATTGGACTG 10363

Qy 429 gtaagttc 436
||| |||
Db 10362 GTAACCTT 10355

RESULT 5
US-09-815-264-77542/c

```
; GENERAL INFORMATION:
;
; APPLICANT: Boukharov, Andrey A.
;
; APPLICANT: Cao, Yongwei
;
; APPLICANT: Cao, Yongwei
```

```
; APPLICANT: Koshi, Jeffrey M.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Nishioka, Tetsuya
```

; APPLICANT: Wu, Wei
 ; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
 ; FILE REFERENCE: 38-21(51237)G
 ; CURRENT APPLICATION NUMBER: 38/000,815 364

: CURRENT FILING DATE: 2001-03-23
 : PRIOR APPLICATION NUMBER: US 09/620,392
 : PRIOR FILING DATE: 2000-07-19
 : PRIOR APPLICATION NUMBER: US 00/700,124

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: PRIOR FILING DATE: 2000-10-31
:
: NUMBER OF SEQ ID NOS: 109669
:
: SEQ ID NO 77542
:
: LENGTH: 21414

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; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-77542

```

Query Match	18.7%;	Score 187.2;	DB 31;	Length 21414;
Best Local Similarity	71.5%;	Pred. No. 3.1e-34;		
Matches 306;	Conservative 0;	Mismatches 108;	Indels 14;	Gaps 4;

10778 GAACCCACACACTGTACTTATTCACAGATATGTAATGATTTATGCTCTGCACAGACCGG 10719

78 caacccttcgcattgcatcgtgcatagataacataaatagatcagcgctgtcaccatg 137
10718 CAACACCTAGCATTTGATCGTGGATAGCATTTGCATTAATAATGATTAGACTTATCACCATGG 10659

138 gtttagtggtgaagcgtatcttaactcatggaatgaagttbgygcacccgtgcagt 197
 10658 ggttagagagagaagcgtatcttaactcatggaatgaagttbgygcacccgtgcagt 10599

y
 198 cttacaacattatgcatctcgcgatgttgtaattactgt-----aatcgaaac 248
 ||| ||| | | | | | | | | |
 b 10598 TTTAATAACAAATCCACACACCAGCTTGTGTTCTATTATTAACAATTCATTCATGATGA 10539

249 catgccttcttcacacatgtatgatatglaatcgttgctcccaaggaaggtaa 308
|| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
10538 CAATGGTCTTGTCACACTAGATTGTTTCGGGAACAATTTGGCTT --- AAAGGCCATTGAT 10482

309 ctctattacttgcgaatgatatatttccaagagcccaaaactctccaacg 368
y ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
10481 CTACCTTTTATTTGCGAATGATGTATTTCGAAGAGCTCCACAAGTACTTCAATG 10422

369 gcaaaattctccccctgtaataatacaatagttatgataaatgcgcgcgtgaatttgatct 428
10421 GTAAA-TTCATCCACGGAATATACACACGTTATGATAAATGCCGTCGAAAGATTGGACCTG 10363

Y 429 gtaagltt 436
||| |||
b 10362 GTACTTT 10355

RESULT 6
S-60-325-448-3410

GENERAL INFORMATION:
APPLICANT: Budworth, P.R.
APPLICANT: Moughamer, T.G.

FILE REFERENCE: 1360.026PRV
CURRENT APPLICATION NUMBER: US/60/325,448
CURRENT FILING DATE: 2001-09-26

SEQ ID NO 3410
LENGTH: 1119
TYPE: DNA

S-60-325-448-3410

Best Local Similarity 98.7%; Pred. NO. 2.5e-22;
Matches 148; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

b
229 aggaatgtatgatctcatgcctgtatagcctcaactccctcgatctgctgca 288
|||||
100

289 tagcatcacaaatgatacagctgtgcaccatggttagtggtgaagctatctta 348

b 349 acttcattggaatgatttggcatcctg 378

	Query Match	Similarity	Score	ID	Length
Best Local	147	96.0%	13.5%	DB 11	2853
Matches	147	Conservative	0	Mismatches	2
				Indels	1
				Gaps	1
QY	43	aggaatcatgatgattcattcagctctcgatagag-cttcaactcttcgcatgatcgtgaca	101		
DB	1859	AGGATATGATATATTTCACGGCTCTGGAGTAGGCCCTTCAACTCTCTGCATATGATCGGGCA	1918		
QY	102	tggattacataaaatgacatgacagctctgtaccatgaggtttaggttggtgaaggtactactta	161		

```

Db      1919 TAGCATTTACATTAATAATGATCAGCGCTTGTCACCACTGGGTATTAGTGTGTAAGAAGCATATCTTA   1978
|||||
QY      162 actcatcggaatatgattggcactctg 191
|||||
Db      1979 ACTTCATGGGAATGAGTTTGCCATCCTG 2008
|||||

RESULT      8
US-09-609-040-3
; Sequence 3, Application US/09609040
; GENERAL INFORMATION:
; APPLICANT: Milimitzer, et al.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE COMPOSITION IN PLANTS
; FILE REFERENCE: 514413-3515.1
; CURRENT APPLICATION NUMBER: US/09/609,040
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: PCT/EP92/00302
; PRIOR FILING DATE: 1992-02-11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2853
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (313)..(2499)
; OTHER INFORMATION: BRANCHING ENZYME
US-09-609-040-3

Query Match          13.5%; Score 134.8; DB 23; Length 2853;
Best Local Similarity 98.0%; Pred. No. 8.le-22;
Matches 147; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      43 aggatatgtatgatttcacgtgcctcgtgatagg-cltcaactcttcgcatgtatgagca 101
|||||
Db      1859 aggatagtatgatttcacgtgcctcgtgataggcccttcaactcctcgcatgtatgagca 1918
|||||
QY      102 tagcttcacataaaatgctacaagctctgcaccatagtggttttagtgttaagaagtactcta 161
|||||
Db      1919 tagcttcacataaaatgcatcagagctctgcaccatagtggttttagtgttaagaagtactcta 1978
|||||
QY      162 actcatcggaatatgattggcactctg 191
|||||
Db      1979 actcatcggaatatgattggcactctg 2008
|||||

RESULT      9
US-09-887-272A-4612
; Sequence 4612, Application US/09887272A
; GENERAL INFORMATION:
; APPLICANT: Hou, Yu-Ming.
; APPLICANT: Quan, Sheng
; APPLICANT: Chang, Hur-Song
; APPLICANT: Zhu, Tong
; APPLICANT: Whitham, Steve
; APPLICANT: Goff, Steve
; APPLICANT: Glazebrook, Jane
; APPLICANT: Chen, Wenguoling
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Xie, Zhiyi
; APPLICANT: Tao, Yi
; APPLICANT: Zou, Guangzhou
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: PLANT GENES INVOLVED IN DEFENSE AGAINST PATHOGENS
; FILE REFERENCE: 1360.003US2
; CURRENT APPLICATION NUMBER: US/09/887,272A
; CURRENT FILING DATE: 2001-06-23
; PRIOR APPLICATION NUMBER: 60/213,634

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; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/214,926
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/261,320
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/264,353
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/273,879
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 09/887,271
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 6813
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4612
; LENGTH: 2655
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-887-272A-4612
```

```
Query Match          12.2%; Score 128.8; DB 33; Length 2655;
Best Local Similarity 84.8%; Pred. No. 2.2e-20;
Matches 156; Conservative 0; Mismatches 27; Indels 1; Gaps 1;
```

```
OY 9 agaacagcatgaacatacaagctctcttctgtcagagatatgtatgttcatcgtctctg 68
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1975 acaatgcaccgagatattcattccttctcatgcatgatatgtatgtattatgctcta 2034

OY 69 gatagc-cttcaactcttcctcatgctcgtgcagcatagcatataaataagcagctt 127
    || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2035 gacagaccttcaacaacctgcgactgacggtgagatagcatataaataagcagctc 2094

OY 128 gtccacctgttttagtctgtgtgaagctatcttaactcattcattggaagattgggcat 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2095 gtccacctgtgtcttaggaaggagagctatcttaattcattcattggaagattgggcat 2154

OY 188 cctg 191
    |||||
DB 2155 cctg 2158
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```
RESULT 10
US-09-304-517A-91564
; Sequence 91564, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 91564
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Zea mays
US-09-304-517A-91564
```

```
Query Match          12.2%; Score 122; DB 17; Length 420;
Best Local Similarity 92.7%; Pred. No. 5.7e-19;
Matches 139; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
```

```
OY 43 aggatatgtatgtattcattgctctgtgataag-cttcaactcttcgcatgtatcgtgca 101
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 aggatatgtatgtattcattgctctgtgacagccttcaacgcttcgcatcgtctgtgga 139

OY 102 tagcattacataaataatgacagcctgttcaccatggttttagtgggtgaaggtcatctta 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 140 tagcattacataaataatgacagcctgttcaccatggttttagtgggtgaaggtcatctta 199

OY 162 acttcattggaatgagtttgggcatcctg 191
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
DB 200 attcattggaatgagtttgggcatcctg 229
```

```
RESULT 11
US-09-985-678-91564
; Sequence 91564, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 91564
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Zea mays
US-09-985-678-91564
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Query Match          12.2%; Score 122; DB 36; Length 420;
Best Local Similarity 92.7%; Pred. No. 5.7e-19;
Matches 139; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
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OY 43 aggatatgtatgtattcattgctctgtgataag-cttcaactcttcgcatgtatcgtgca 101
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 aggatatgtatgtattcattgctctgtgacagccttcaacgcttcgcatcgtctgtgga 139

OY 102 tagcattacataaataatgacagcctgttcaccatggttttagtgggtgaaggtcatctta 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 140 tagcattacataaataatgacagcctgttcaccatggttttagtgggtgaaggtcatctta 199

OY 162 acttcattggaatgagtttgggcatcctg 191
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 200 attcattggaatgagtttgggcatcctg 229
```

```
RESULT 12
US-09-394-745-21714
; Sequence 21714, Application US/09394745
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lajudi, Raghuath V.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI
; FILE REFERENCE: 38-21(15454)B
; CURRENT APPLICATION NUMBER: US/09/394,745
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 57264
; SEQ ID NO 21714
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3062-002-Q1-K2-E10
US-09-394-745-21714
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Query Match          12.2%; Score 122; DB 17; Length 421;
Best Local Similarity 92.7%; Pred. No. 5.7e-19;
Matches 139; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
```

```
OY 43 aggatatgtatgtattcattgctctgtgataag-cttcaactcttcgcatgtatcgtgca 101
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 81 aggatatgtatgtattcattgctctgtgacagccttcaacgcttcgcatcgtctgtgga 140

OY 102 tagcattacataaataatgacagcctgttcaccatggttttagtgggtgaaggtcatctta 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 141 tagcattacataaataatgacagcctgttcaccatggttttagtgggtgaaggtcatctta 200

OY 162 acttcattggaatgagtttgggcatcctg 191
```


GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 09:13:22 : Search time 643.61 seconds
(without alignments)
4921.411 Million cell updates/sec

Title: US-09-508-377-10_COPY_9500_10500
Perfect score: 1001
Sequence: 1 tcgcagacatagaacagcatga.....ctggagcaatagctttttt 1001

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2084544 seqs, 1582152599 residues
Total number of hits satisfying chosen parameters: 4169088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing First 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/prodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/prodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/prodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/prodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/prodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	13.0	2554	7 US-10-162-948-1	Sequence 1, Appl
2	122	12.2	3144	8 US-60-391-781-685	Sequence 685, App
3	110.8	11.1	2443	8 US-60-368-387-1	Sequence 1, Appl
4	110.8	11.1	2443	8 US-60-381-534-1	Sequence 1, Appl
5	110.8	11.1	2919	8 US-60-391-781-709	Sequence 709, App
6	102.6	10.2	786	8 US-60-391-781-2614	Sequence 2614, App
7	93.6	9.4	3003	7 US-10-056-454A-12	Sequence 12, Appl
8	92.8	9.3	2529	7 US-10-056-454A-17	Sequence 17, Appl
9	92	9.2	3033	7 US-10-056-454A-14	Sequence 14, Appl
10	90.4	9.0	2576	7 US-10-056-454A-16	Sequence 16, Appl
11	90.4	9.0	2578	7 US-10-056-454A-19	Sequence 19, Appl
12	90.4	9.0	2975	7 US-10-056-454A-13	Sequence 13, Appl
13	90.4	9.0	3231	7 US-10-056-454A-18	Sequence 18, Appl
14	90	9.0	1867	6 US-10-219-999-3997	Sequence 3997, App
15	67.4	6.7	2096	6 US-10-213-073-149	Sequence 149, App
16	67.4	6.7	2913	1 PCT-US02-18947-442	Sequence 442, App
17	67.4	6.7	2913	1 PCT-US02-18947-442	Sequence 442, App
18	67.4	6.7	2955	1 PCT-US02-25766-8907	Sequence 8907, App
19	60.8	6.1	4563	1 US-10-110-777-1	Sequence 1, Appl
20	59.2	5.9	2324	6 US-10-219-999-16451	Sequence 16451, A
21	59.2	5.9	2551	8 US-60-368-387-2	Sequence 2, Appl
22	59.2	5.9	2551	8 US-60-381-534-2	Sequence 2, Appl
23	54.8	5.5	2007	7 US-10-179-131-2516	Sequence 2516, App
24	53.6	5.4	1941	8 US-60-360-039-33970	Sequence 33970, A
25	53.4	5.3	2638	8 US-60-360-039-27656	Sequence 27656, A

26	51.2	5.1	2115	8 US-60-360-039-25407	Sequence 25407, A
27	50.8	5.1	189	5 US-09-975-254-16738	Sequence 16738, A
28	50.6	5.1	184	5 US-09-975-254-29078	Sequence 29078, A
29	42.4	4.2	5525	7 US-10-172-086-8	Sequence 8, Appl
30	41.6	4.2	2025	5 US-09-540-2098-375	Sequence 375, App
31	41.6	4.2	96589	6 US-10-035-832-1226	Sequence 1226, App
32	41.6	4.2	96589	6 US-10-052-482-214	Sequence 214, App
33	40.8	4.1	6246	7 US-10-172-086-28	Sequence 28, Appl
34	40.6	4.1	2132	7 US-10-099-278-39	Sequence 39, Appl
35	39.4	3.9	2140405	7 US-10-027-632-76212	Sequence 76212, A
36	38.8	3.9	1669	5 US-09-591-466C-1	Sequence 1, Appl
37	38.6	3.9	500	5 US-09-991-936-601	Sequence 601, Appl
38	38.6	3.9	839	7 US-10-155-881-14448	Sequence 14448, A
39	38.4	3.8	2601	7 US-10-179-131-2345	Sequence 2345, App
40	37.8	3.8	2635	7 US-10-105-299-8524	Sequence 8524, App
41	37.6	3.8	4238	6 US-10-205-219-152	Sequence 152, App
42	37.4	3.7	310	7 US-10-102-524-1616	Sequence 1616, App
43	37.2	3.7	1191139	5 US-09-811-352B-1	Sequence 1, Appl
44	37.2	3.7	1191139	7 US-10-140-924-1	Sequence 1, Appl
45	37.2	3.7	1691139	7 US-10-067-514-1	Sequence 1, Appl

ALIGNMENTS

```

RESULT 1
US-10-162-948-1
; Sequence 1, Application US/10162948
; GENERAL INFORMATION:
; APPLICANT: Jane, Jay-Jin
; APPLICANT: Mou, Belgium
; APPLICANT: Jansson, Christer
; APPLICANT: Sun, Chuanxin
; TITLE OF INVENTION: TRANSGENIC CORN PLANTS HAVING SEEDS WITH MODIFIED
; TITLE OF INVENTION: CORNSARCH CHARACTERISTICS AND METHOD OF MAKING THE
; FILE REFERENCE: 480927, 90081
; CURRENT APPLICATION NUMBER: US/10/162, 948
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/295, 649
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2554
; TYPE: DNA
; ORGANISM: Hordeum vulgare
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(2208)
US-10-162-948-1

Query Match 13.0%; Score 130; DB 7; Length 2554;
Best Local Similarity 96.0%; Pred. No. 5.5e-23;
Matches 144; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 43 aggaatgatgatgttcacgtcctcgtatag-gcttaactcttcgcatgtgagca 101
|||||
DB 1568 aggaatgatgttcacgtcctcgtatag-gcttaactcttcgcatgtgagca 1627
|||||

QY 102 taacattacataaagaatcagctgttcacatggtttaggtgtgaagctactta 161
|||||
DB 1628 taacattacataaagaatcagctgttcacatggtttaggtgtgaagctactta 1687
|||||

QY 162 actcatggaatgagtttgagctcctg 191
|||||
DB 1688 attcatggaatgagtttgagctcctg 1717
|||||

RESULT 2
US-60-391-781-685
; Sequence 685, Application US/60391781

```

```

: GENERAL INFORMATION:
: APPLICANT: Laurie, Cathy C.
: TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
: FILE REFERENCE: 38-77(52900)B
: CURRENT APPLICATION NUMBER: US/60/391,781
: CURRENT FILING DATE: 2002-06-25
: PRIOR APPLICATION NUMBER: 60/365,301
: PRIOR FILING DATE: 2002-03-15
: NUMBER OF SEQ ID NOS: 3034
: SEQ ID NO 685
: LENGTH: 3144
: TYPE: DNA
: ORGANISM: Zea mays
: US-60-391-781-685

```

Query Match	12.2%	Score 122;	DB 8;	length 3144;
Best Local Similarity	92.7%	Pred. No. 6.3e-21;		
Matches 139;	Conservative	0;	Mismatches 10;	Indels 1;
			Gaps	1

QY 43 aggatatgatgatattcattcagctctcggatag-cttcaactcttcgcatctgacgtgca 101
|||||
Db 2107 aggatatgatgatattcattcagctctcggacagccttcaacgctcgtcagtcgttgga 2166
|||||

QY 102 tagcattacaataaattgatacagctgtgcaccatggtttagtgctggaagcctatctta 161
|||||
Db 2167 tagcattacaataaattgatacagctgtgcaccatggtttagtgagtggaagcctatctta 2226
|||||

```
QY      162  actlcatggaatgaglttggcaccctg 191
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2227 attcatggaatgaglttggcaccctg 2256
```

```

RESULT 3
US-60-368-387-1
: Sequence 1, Application US/60368387
: GENERAL INFORMATION:
: APPLICANT: Pearlstein, Richard W.
: APPLICANT: Broglio, Karen E.
: APPLICANT: Hines, Christopher F.
: TITLE OF INVENTION: Maltize Starch Containing Elevated Amounts of Actual Amylose
: FILE REFERENCE: BB1510PRV
: CURRENT APPLICATION NUMBER: US/60/368,387
: CURRENT FILING DATE: 2002-03-27
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 1
: LENGTH: 2443
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(2443)
: OTHER INFORMATION: SBEII modified region
: US-60-368-387-1

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Query Match	11.1%;	Score 110.8;	DB 8;	Length 2443;
Best Local Similarly	88.08;	Pred. No. 4.1e-18;		
Matches 132; Conservative	0;	Mismatches 17;	Indels 1;	Gaps 1;

QY 43 aggaatatgatgatattcaatgcgtctgataag-gcttcaacctcttcgcatgtagctgtgca 101
|||||
Db 1411 aggaatatgatgatattcaatgcgtctgataag-gcttcaacctcttcgcatgtagctgtgca 1470

[illegible]

```

Oy      162  acttcattgggaatgagtttgggcatcctg  191
          |  ||||| ||||| ||||| ||||| |||||
Db      1531  atttcattgggaatgagtttgggcatcctg  1560

```

RESULT 4
US-60-381-534-1
; Sequence 1, Application US/60381534

APPLICANT: Brogile, Karen E.
APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose
FIR REFERENCE: 0819067

```

; CURRENT APPLICATION NUMBER: 05/60/381,534
;
; CURRENT FILING DATE: 2002-05-16
;
; NUMBER OF SEQ ID NOS: 6
;
; SOFTWARE: PatentInversion 3.1

```

```

; SEQ ID NO 1
;
; LENGTH: 2443
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1).(2443)
; OTHER INFORMATION: SBREIT modified region

```

US-60-361-534-1

Query Match 11 1%: score 110

Query Match	11.1%	Score 110.8;	DB 8;	Length 2443;
Best Local Similarity	86.0%;	Pred. No. 4.1e-18;		
Matches 132;	Conservative 0;	Mismatches 17;	Indels 1;	Gaps 1;
OY	43	aggatggtatgatttcacgctctgtagag-gcttcaactcttcgcatgttcgtgca	101	

QY	102	tagcattacataaaatgatacgaagctgtgcaacatggttttagtggttgaaagctatctta	161
Db	1471	tagcattacataaaatgatacgaattacccaatggttttagtgagagagagggctatctta	1530
QY	43	aggatatacgaattcaatgagctctggatgagtgcttcaactcttcgaattatctgttcca	100
Db	1411	aggatatacgaattcaatgagcctcgatagacattccaactcctaacttgaatgtgtgga	1470/1

QY 162 attcatggygaatgagtttggcacctg 191
| |||||
Db 1531 attcatggygaatgagtttggcacctg 1560

```

RESULT      5
US-60-391-781-709
: Sequence 709, Application US/60391781
:
: GENERAL INFORMATION:
: APPLICANT: Laitrie, Cathy C.
: TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
: FILE REFERENCE: 38-77(52900)B
: CURRENT APPLICATION NUMBER: US/60/391,781
: CURRENT FILING DATE: 2002-06-25
: PRIOR APPLICATION NUMBER: 60/365,301
: PRIOR FILING DATE: 2002-03-15
: NUMBER OF SEQ ID NOS: 3034
:
: SEQ ID NO 709
: LENGTH: 2919
: TYPE: DNA
: ORGANISM: Zea mays
:
US-60-391-781-709

```

Query Match	11.1%	Score 110.8;	DB 8;	Length 2919;
Best Local Similarity	86.0%;	Pred. No. 4.3e-18;		
Matches 132; Conservative	0;	Mismatches 17;	Indels 1;	Gaps 1;

```
QY      43 aggatatgtatgattcatgcctcgtatag-gcttcaactcttcgaattgacgtggca 101
        |||||||
Db    1906 aggaatatgtatgattcatgcctcgtatagaaccttcaactcttacattgactcgtyga 1965
```

QY 102 tagcattacataaagatgacagcctgttcacacatgggtttagtggtaaggctatctta 161
|||||
Db 1966 tagcattacataaagatgattagacttatcacaaatgggttttaggaaggagggctatctta 2025
|||||

Qy	162	acttcatggaatgagtttggcatcctg	191
Db	2026	attcatggaatgagtttggcatcctg	2055

```

RESULT      6
US-60-391-781-2614/C
; Sequence 2614, Application US/60391781
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C.
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Oil in Plants
; FILE REFERENCE: 38-77(52900)B
; CURRENT APPLICATION NUMBER: US/60/391,781
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/365,301
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 3034
; SEQ ID NO 2614
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(786)
; OTHER INFORMATION: unsure at all n locations
; US-60-391-781-2614

```

Query Match	10.2%	Score 102.6	DB 8	Length 786
Best Local Similarity	80.5%	Pred. No. 3.6e16		
Matches 120; Conservative	0	Mismatches 29	Indels 0	Gaps 0

Qy	563	aaataatcatgattttttgtcagggagatgcagatatttcttagatatcogtgtgtcaaga	642
Db	409	ACAAATTTTAATCCCTTTTTCAGGGAGATGAGATTATCTTAGATATCGTGTGTCAGAG	350
Qy	643	gttcgatcagcgaatgcagatctctgtggaaaaatatgggtatgtaaccggtttcct	702
Db	349	GTTTGACCAAGGCATGAGCACCTTGAGGGGAAATATCAAGATGTGCACGTGTTATCTC	290
Qy	703	tgttcgataacagtcacagtttaagtc	731
Db	289	TGTTGCACAATTACTTAACCACTTAATTTTC	261

RESULT 7
US-10-056-454A-12
Sequence 12, Application US/10056454A
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unidigma Blvd.
CITY: Newcastle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3003 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

```

;      SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-056-454A-12

```

[illegible]

RESULT 8
 US-10-056-454A-17
 ; Sequence 17, Application US/10056454A .
 ; GENERAL INFORMATION:
 ; APPLICANT: National Starch and Chemical Investment Holding Corporation
 ; TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: National Starch and Chemical Investment Holding Corporation
 ; STREET: 1000 Unidigma Blvd.
 ; CITY: Newcastle
 ; STATE: Delaware
 ; COUNTRY: United States of America
 ; ZIP: 19720
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/056,454A
 ; FILING DATE: 25-Jun-2002
 ;
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2529 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ;
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-10-056-454A-17

Query Match	9.3%	Score 92.8	DB 7	Length 2529
Best Local Similarity	76.9%	Pred. No. 1.6e-13		
Matches 123	Conservative	2	Mismatches 34	Indels 1
				Gaps 14
QY	33	cccttgagcaagatagatgatattcagagctcggatag-ggtccaactctcgact	91	
DB	1838	CTGATGGACAGAGATATGATATTTTATGCTCTGGATAGACCGYCAACATTAATA	1897	
QY	92	gatcgtggcatgacatcatcataaaatgacagcctgttcacacatggttaagtgtgaa	151	
DB	1898	GATCGTGGGATATGACATTCGACAAAGATGATTAGCGTTTGATATAGGAGATAGAGAGAA	1957	
QY	152	ggctatcttaacttcacatgggaaatgagtgttggcaactcg	191	
DB	1958	GGGTACTTAATTTTCATGGGAATGAATTCGGCCACCTTG	1997	

RESULT 9
 US-10-056-454A-14
 : Sequence 14, Application US/10056454A

RESULT 9
US-10-056-454A-14
; Sequence 14, Application US/10056454A

GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Unigema Blvd.
CITY: Newcastle
STATE: Delaware
COUNTRY: United States of America
ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 145..2790
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-056-454A-14

Query Match	9.2%	Score 92;	DB 7;	Length 3033;
Best Local Similarity	77.5%;	Pred. No. 2.6e-13;		
Matches 124;	Conservative 0;	Mismatches 35;	Indels 1;	Gaps 1;
QY	33	ctcttgcgcagagatgataatgattcattgcctgcgtatag-gcttcaactcttcgacat	91	
Db	2068	CTGATGAGCAAGAGATATGTATGATTTTATGGCTCTGGATAGACCTCAACATCATTTAATA	2127	
QY	92	gacgtgycatagcatcatcaataaataatgcagcgcctgtccacatagtggttagtgatgaa	151	
Db	2128	GATCGTGGGATAGCATTCACACAAGATGATTTAGGCTTTGTAACATATGGATTAGAGAGAGA	2187	
QY	152	ggctatcttaacttcattgaggaatagatttgggactctg	191	
Db	2188	GGGTACCTTAATTTTCATGTGGGAATTAATTTGGCCACCCTCG	2227	

RESULT 10
 US-10-056-454A-16
 : Sequence 16, Application US/10056454A
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: National Starch and Chemical Investment Holding Corporation
 : TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
 : NUMBER OF SEQUENCES: 20
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: National Starch and Chemical Investment Holding Corporation
 : STREET: 1000 Unilegma Blvd.
 : CITY: Newcastle
 : STATE: Delaware
 : COUNTRY: United States of America
 : ZIP: 19720
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/10/056,454A
 : FILING DATE: 25-Jun-2002
 :
 : INFORMATION FOR SEQ ID NO: 16:
 : SEQUENCE CHARACTERISTICS:

```

:      LENGTH: 2576 base pairs
:      TYPE: nucleic acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
:      SEQUENCE DESCRIPTION: SEQ ID NO: 16
US-10-056-454A-16

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Query Match	9.0%;	Score 90.4;	DB 7;	Length 2576;
Best Local Similarity	76.9%;	Pred. No. 6.3e-13;		
Matches 123;	Conservative 0;	Mismatches 36;	Indels 1;	Gaps 1;

OY 33 cttcttcttggaagatattgtagtttcacggccgcgtgatag -gtctcaacccttcgactt 91
 || | | | | | | | | | | | | | | | | | | |
Db 1843 CTGATGGACAAGGATTATGTATGATTTTAAAGCTCTGGATAGACCGCAACATCATTAATA 1902

OY 92 gatcgtgcatacatcataaaatcgatcagaactgtcacatggttaagtgttaa 151
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Db 1903 GATGCTGGGTAGCATTGCCAAGATGATTAGGCTTGTACTATATGGATTAGGAAGAGAA 1962

OY 152 ggcatacttaactcatgagganaatgtagtttggtgacacctg 191
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Db 1963 GGGTACTTAATTTTCATGGGAAATGATATTCGGCACCCCTG 2002

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Query Match	9.0%	Score 90.4	DB 7	Length 2578
Best Local Similarity	76.9%	Pred. No. 6.3e+13		
Matches 123	Conservative 0	Mismatches 36	Indels 1	Gaps 1

QY	33	ctctttgtgcaggatatlgaatttcacatggtcctcgtatag-ggttccaactcttcgalt	91
Db	1845	CTGATGAGCAGAGATATGATGATTTTATGGCTCTGATAGACCGCAACATCATTAATA	1904
QY	92	gatcgttgcataagcatlcaataaaatgcatcagcgttgcacatggttttggttggtgta	151
Db	1905	GATCGTGGGATAGCATTCACACAAAGATGATTGAGCTTGTAACATATGAGTATAGGAGAGAA	1964
QY	152	ggctatcttaactcatgcatgggaattagtttgggcatctcg	191
Db	1965	GGGTACCTAAATTTTCATGGAGAAATTAATTCGGCCACCCCG	2004

RESULT 12
US-10-056-454A-13
; Sequence 13, Application US/10056454A
; GENERAL INFORMATION:
; APPLICANT: National Starch and Chemical Investment Holding Corporation
; TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: National Starch and Chemical Investment Holding Corporation
; STREET: 1000 Unigema Blvd.
; CITY: Newcastle
; STATE: Delaware
; COUNTRY: United States of America
; ZIP: 19720
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,454A
; FILING DATE: 25-Jun-2002
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2975 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-056-454A-13

Query Match 9.0%; Score 90.4; DB 7; Length 2975;
Best Local Similarity 76.9%; Pred. No. 6.6e-13;
Matches 123; Conservative 0; Mismatches 36; Indels 1; Gaps 1;
QY 33 cctcttgacagatattatgattcgtctgtagatg-gcttcaactcttcgcat 91
DB 2066 CTGATGACAAAGATATGATATTTATGCTCTGGATAGACCCCAACATCATTAATA 2125
QY 92 gatcgtgcatagcattacataaataatgacagctgttcacacatggttagtgtaa 151
DB 2126 GATCGTGGGATGATGATGACAAAGATGATTAAGCTTGTACATGAGATTAGAGAGAGA 2185
QY 152 ggcatacttaacttcattcagggaatgagttgggcatcctg 191
DB 2186 GGGTACCTAAATTCATGGGAATGATTCGGCCACCCCTG 2225
RESULT 13
US-10-056-454A-18
; Sequence 18, Application US/10056454A
; GENERAL INFORMATION:
; APPLICANT: National Starch and Chemical Investment Holding Corporation
; TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: National Starch and Chemical Investment Holding Corporation
; STREET: 1000 Unigema Blvd.
; CITY: Newcastle
; STATE: Delaware
; COUNTRY: United States of America
; ZIP: 19720
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,454A
; FILING DATE: 25-Jun-2002
; INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 3231 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-056-454A-18

Query Match 9.0%; Score 90.4; DB 7; Length 3231;
Best Local Similarity 76.9%; Pred. No. 6.8e-13;
Matches 123; Conservative 0; Mismatches 36; Indels 1; Gaps 1;

QY 33 cctcttgacagatattatgattcgtctgtagatg-gcttcaactcttcgcat 91
DB 2151 CTGATGACAAAGATATGATATTTATGCTTGGATAGACCGTCAACATCATTAATA 2210
QY 92 gatcgtgcatagcattacataaataatgacagctgttcacacatggttagtgtaa 151
DB 2211 GATCGTGGGATGATGATGACAAAGATGATTAAGCTTGTACATGAGATTAGAGAGAGA 2270
QY 152 ggcatacttaacttcattcagggaatgagttgggcatcctg 191
DB 2271 GGGTACCTAAATTCATGGGAATGATTCGGCCACCCCTG 2310

RESULT 14
US-10-219-999-3997
; Sequence 3997, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-106527260C
; CURRENT APPLICATION NUMBER: US/10/219,999
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/312,544
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 3997
; LENGTH: 1867
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(1268)
; OTHER INFORMATION:
US-10-219-999-3997

Query Match 9.0%; Score 90; DB 6; Length 1867;
Best Local Similarity 79.3%; Pred. No. 7.3e-13;
Matches 119; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

QY 43 aggatatgatattcattcaggtctcgtagatg-gcttcaactcttcgcatgtagtgca 101
DB 550 aggatatgatattcattcaggtctcgtagatg-gcttcaactcttcgcatgtagtgca 609
QY 102 tagcatlacataaataatgacagctgttcacacatggttagtgtagaagctactcta 161
DB 610 tagcgttgacaaaatgattagcttatlacacatggttcttggttgtagaaggtatttaa 669
QY 162 actcatcagggaatgagttgggcatcctg 191
DB 670 atttatgggaatgattggtgcacatcctg 699

```
RESULT 15
US-10-213-073-149
; Sequence 149, Application US/10213073
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: p213ACIN
; CURRENT APPLICATION NUMBER: US/10/213,073
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 09/760,483
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
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; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
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; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
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; PRIOR FILING DATE: 2000-09-14
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; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
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Query Match 6.7%; Score 67.4; DB 6; Length 2096;
Best Local Similarity 73.5%; Pred. No. 4.2e-07;
Matches 86; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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DB 786 ctttaactcagctatgtatcgtaagatacagcttcataaagtaltcgaactcattacgc 845
QY 135 tgggttaagtgtgaagctatcttaactcatggaataatgatttggcatcctg 191
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DB 846 atgggctgtgtgagaagcattcctaattcatgtgtatgaatttggcatcctg 902
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 01:43:32 : Search time 3917.59 Seconds
(without alignments)
5341.686 Million cell updates/sec

Title: US-09-508-377-10_COPY_1_1000
Perfect score: 1000
Sequence: 1 agaacacccatcatttaga.....acactcccgctgggtccct 1000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Genembl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_com:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	1000	100.0	11463	6	AX031271	Sequence
2	1000	100.0	11475	8	AF38431	Aegilops
3	43.8	4.4	210476	10	AC087166	Mus muscu
4	43.8	4.4	225726	2	AC074328	Mus muscu
5	41.4	4.1	79976	8	AB008264	Arabidops
6	41.4	4.1	96217	9	AC002410	Human BAC
7	40.8	4.1	133021	9	AL161624	Human DNA
8	40.8	4.1	142184	2	AC037428	Homo sapi
9	40.6	4.1	81580	8	AP000736	Arabidops
10	40.6	4.1	98017	8	AC027033	Arabidops
11	40.6	4.1	207872	10	AC074329	Mus muscu
12	40	4.0	65955	8	AP003681	Oryza sat
13	40	4.0	318221	2	PFMAL13P3	Plasmodiu
14	39.8	4.0	7218	6	I66494	Sequence 14
15	39.2	3.9	1055	6	AX083745	Sequence
16	39.2	3.9	161531	2	AC079960	Homo sapi
17	39.2	3.9	170608	2	AL359372	Homo sapi
18	39.2	3.9	171730	2	AL589663	Homo sapi
19	39	3.9	166527	9	AC092057	Homo sapi
20	39	3.9	170682	2	AC109584	Homo sapi
21	39	3.9	190070	2	AC079032	Homo sapi
22	39	3.9	196660	9	AC007000	Homo sapi
23	39	3.9	203426	2	AL645913	Mus muscu
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25	38.8	3.9	207166	2	AC073703	Mus muscu
26	38.6	3.9	102575	2	AL353670	Homo sapi
27	38.6	3.9	103447	2	AC095853	Rattus no
28	38.6	3.9	110000	2	LMFLCHR36_30	Continuatio
29	38.6	3.9	125020	9	AF429315	Homo sapi
30	38.4	3.8	161031	9	AC079610	Homo sapi
31	38.2	3.8	43044	3	AC006730	Caenorhab
32	38.2	3.8	110000	2	AC016150	Homo sapi
33	38	3.8	44067	8	AL357136	Human DNA
34	38	3.8	57047	8	LES03345	Lycopersi
35	38	3.8	168834	2	AC096984	Rattus no
36	38	3.8	169281	9	AC0079232	Homo sapi
37	38	3.8	179637	2	AC007961	Mus muscu
38	38	3.8	205884	3	AC068241	Mus muscu
39	37.8	3.8	33995	3	CEK11E4	Caenorhabd
40	37.8	3.8	34175	9	CNS001VB	Al096805
41	37.8	3.8	111119	2	AL162741	Homo sapi
42	37.8	3.8	116376	2	AL139287	Homo sapi
43	37.8	3.8	133769	9	AC010429	Homo sapi
44	37.8	3.8	152116	9	AC008471	Homo sapi
45	37.6	3.8	1141	6	AX083744	Sequence

ALIGNMENTS

RESULT 1
AX031271 LOCUS AX031271 11463 bp DNA
DEFINITION Sequence 10 from Patent W09914314.
AX031271
ACCESSION AX031271
VERSION AX031271.1 GI:10278663
KEYWORDS
SOURCE
ORGANISM Aegilops tauschii.
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Aegilops.
1 (bases 1 to 11463)

REFERENCE
AUTHORS Li,Z., Morell,M. and Rahman,S.
TITLE Regulation of gene expression in plants
JOURNAL Patent: WO 9914314-A 10 25-MAR-1999;
GOODMAN FIELDER LTD (AU) ; LI ZHONGYI (AU) ; MORELL MATTHEW (AU) ;
RAHMAN SADEOUR (AU) ; UNIV AUSTRALIAN (AU) ; COMMW SCIENT IND RES
ORG (AU) ; GROUPE LIMAGRAIN PACIFIC PTY L (AU)
FEATURES
source
1. 11463
Location/Qualifiers
/organism="Aegilops tauschii"
/db_xref="taxon:37682"

JOURNAL TITLE	Genome Therapeutics Corporation Sequencing Center: Mouse Genome		
REFERENCE	Sequence Data		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 225726)		
JOURNAL	Smith,D.R.		
	Direct Submission		
	Submitted (23-AUG-2000) Genome Therapeutics Corporation, 100 Beaver		
	Street, Waltham, MA 02453, USA		
COMMENT	On Jan 15, 2002 this sequence version replaced gi:15208553.		

	Genome Center		
	Center: Genome Therapeutics Corporation		
	Center code: GTC		
	Web site: http://www.genomecorp.com/		
	Contact: gtc-seqcenter@genomecorp.com		

	Project Information		
	Center project name: mp042		

	Summary Statistics		
	Sequencing vector: N/A		
	Chemistry: dye-terminator Big Dye; 100% of reads		
	Assembly program: Phrap; version 990315		
	Consensus quality: 225213 bases at least Q40		
	Consensus quality: 225480 bases at least Q30		
	Consensus quality: 225564 bases at least Q20		
	Insert size: 225825; sum-of-contigs		
	Quality coverage: 6.6x in Q20 bases; sum-of-contigs		

FEATURES	* NOTE: This is a 'working draft' sequence. It currently		
source	* consists of 1 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
	1 225726: contig of 225726 bp in length.		
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	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/chromosome="12"		
	/clone="RP23-101G12"		
	/clone_lib="RPCI-23"		
	1..225726		
	/note="assembly_name:Contig2		
	clone_end:SP6"		
BASE COUNT	70130 a 43240 c 44470 g 67886 t		
ORIGIN			
	Query Match 4.4%; Score 43.8; DB 2; Length 225726;		
	Best Local Similarity 55.6%; Pred. No. 0.31; 67; Indels 0; Gaps 0;		
	Matches 84; Conservative 0; Mismatches 67; Indels 0; Gaps 0;		
QY 309	tgaacacatgatgtatcatcagccctgattgaggaagcaacatgcctttccct 368		
Db 38555	TAAAGAAATGATGCGACAACTTACCCATCTGTATGGGACACATGAAGAATTTCTACG 38496		
QY 369	ctggaattcatagtcatcactttttttaatggaagcaagattggcaaacatgcat 428		
Db 38495	AGGAAACTCATGTAGCTGACAGCTGTACAAAAAGAACTAGAGAAACACACACTAGCAG 38436		
QY 429	tttcaaacaggaaatattatctcaacca 459		
Db 38435	CTTGACACATCTACTTAAAGCTCTGAGACAA 38405		
RESULT 5			
LOCUS	AB008264 79976 bp DNA linear PLN 27-DEC-2000		
DEFINITION	Arabidopsis thaliana genomic DNA, chromosome 5, pl clone:MBD2.		
ACCESSION	AB008264.1 GI:2618599		
VERSION			

KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	MEDLINE	REFERENCE	TITLE	JOURNAL	COMMENT
Arabidopsis thaliana (strain:Columbia) DNA, clone_11b:Mitsui P1 clone:MBD2.		Arabidopsis thaliana								
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		Arabidopsis thaliana								
1 (sites)		Nakamura, Y., Sato, S., Kaneko, T., Kotani, H., Asamizu, E., Miyajima, N., and Tsubata, S.								
Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones										
DNA Res. 4 (6), 401-414 (1997)										
98162728										
2 (bases 1 to 79976)										
Nakamura, Y.										
Direct Submission										
Submitted (24-OCT-1997) Yesukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel:81-438-55-3935, Fax:81-438-52-3934)										
Address for correspondence: kaos@kazusa.or.jp										
For the latest information on annotation of this clone, please see										
http://www.kazusa.or.jp/kaos/cgi-bin/seq_graph.cgi?c=MBD2										
Genes with similarity to proteins in the databases are described in										
'product' or 'note' qualifiers. Genes that have no significant										
protein similarity are described as 'unknown protein'.										
The software programs used to predict genes include: Grail										
(Informatics Group, Oak Ridge National Laboratory,										
http://combio.ornl.gov/Grail-1.1.3/).										
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),										
NetGene2 (S.M. Hedsgaard, et al., CBS, Technical University of										
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and										
SplicePredictor (Volker Brendel, Stanford University,										
http://gremlini.zozi.iastate.edu/cgi-bin/sp.cgi).										
Genes encoding tRNAs are predicted by tRNAscan-SE										
(Sean Eddy, Washington university school of medicine, St. Louis,										
http://genome.wustl.edu/eddy/tRNAscan-SE/).										
This sequence may not be the entire insert of this clone. It may be										
shorter because we remove overlaps between neighboring submissions.										
The 5' clone is MJB21 and the 3' clone is MRD20.										
Location/Qualifiers										
1..79976										
/organism="Arabidopsis thaliana"										
/strain="Columbia"										
/db_xref="taxon:3702"										
/chromosome="5"										
/clone="MBD2"										
/clone_lib="Mitsui P1"										
complement(1..218)										
/note="CDS is reported in Acc# AB007647"										
gene_id:MJB21.20"										
/number=1										
/evidence=not_experimental										
/product="v2 snrp auxiliary factor, small subunit"										
join(5306..5761,5932..6828)										
/note="gene_id:MBD2.2"										
/codon_start=1										
/evidence=not_experimental										
/product="N-hydroxycinnamoyl/benzoyltransferase-like										
protein"										
/protein_id="BAB09184.1"										
/db_xref="GI:9758571"										
/translation="MDSSSSKVIYKSKSPVKKTIPEESKOPYIISPMDYAMLSTVOYIQD										
KGLFHKPPLDSDIDLTLEKLDKSLAVTLVHTPIAGRLSLSTLTKPKSYSVFVCDNS										
PGAPFIATSDLCIKDIVGAKVPSIVOSFPDHRKAVHDDHTMSLSVQYGLVDG										
FTGISMNHAMDGTAFWFKFPMASEIIRGQGSNDNDICLNPVLYKRY IDEGVPGLD										
SLPSSHDEPIRTIESPLIKRMFCFSEETIRMLKTRVNOCGTSSISFQSLTAVIIVG										
RCITRRARPLIDRETSCRVADNGRNPPLHKRYFGCGSALRTAKAKGILENDG										
FALKIYQVAEHSTSEKYSQIIDQWLKSPITYIYHIDRLPEPSSVMGSSPPRNKYGCEP										

Db 41154 GAATCAATTC 41164

RESULT 6
AC002410/C 96217 bp DNA linear PRI 04-FEB-2000
LOCUS Human BAC clone CTA-264L19 from 7p15-p21, complete sequence.
DEFINITION AC002410
AC002410 GI:2317822
VERSION HTG.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 96217)
AUTHORS Graves, T., Hinds, K., Sutterer, C. and Biewald, T.
TITLE The sequence of H. sapiens BAC clone CTA-264L19
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1997) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 3 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 4 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 5 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 6 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 7 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 8 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 9 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 10 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 11 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 12 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 13 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 14 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 15 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 16 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 17 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 18 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 19 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 20 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 21 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 22 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 23 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 24 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 25 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 26 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 27 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 28 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 29 (bases 1 to 96217)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

FEATURES
source
This clone contains STS SWSS2954 (NID: g1113657).
actual start of this clone is at base position 63963 of CTB-13P7;
actual end is at 96217 of CTA-264L19. This clone is part of an
unanchored island, orientation is unknown.

Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="7"
/map="7p15-p21"
/clone="CTA-264L19"
/clone_11b="CTB-HS-A"
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/rpt_family="L1"
complement(6410. .6474)
repeat_region
6589. .6632
/rpt_family="L1"
complement(10870
10579. .10870
/rpt_family="ALU"
complement(11846. .11865)
19652. .19944
/rpt_family="L1"
complement(22521. .22610)
22657. .22947
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complement(23151. .23302)
/rpt_family="L1"
complement(23549. .23659)
/rpt_family="L1"
complement(26909. .27202)
/rpt_family="ALU"
complement(28673. .30110)
/rpt_family="L1"
30385. .32264
/rpt_family="L1"
complement(31054. .31464)
/rpt_family="L1"
complement(33330. .33733)
/rpt_family="L1"
complement(39149. .39439)
41105. .41394
/rpt_family="ALU"
43696. .44071
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44234. .44364
/rpt_family="MER"
complement(44458. .44758)
45804. .46080
/rpt_family="ALU"
49078. .49301
/rpt_family="ALU"
complement(54849. .55141)
/rpt_family="ALU"
complement(55314. .55346)
67429. .67457
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complement(73310. .73676)
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complement(79278. .79330)
80325. .80693
/rpt_family="ALU"
complement(85475. .85667)
/rpt_family="MER"

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CHR/> or send an E-mail to egreen@nhgri.nih.gov

SOURCE INFORMATION:
This clone is from a release of the human BAC library. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).
VECTOR: pBelOBAcl1
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is CTB-13P7, 200 bp overlap. The

/note="MIR repeat: matches 30. .262 of consensus"
18803. .19103
repeat_region /note="AluSg repeat: matches 1. .301 of consensus"
19223. .19345
repeat_region /note="L1PA7 repeat: matches 6010. .6141 of consensus"
19470. .19565
repeat_region /note="AluSg/x repeat: matches 212. .307 of consensus"
19571. .19723
repeat_region /note="L2 repeat: matches 2008. .2143 of consensus"
19724. .20154
repeat_region /note="MLT2FB repeat: matches 3. .414 of consensus"
20155. .20431
repeat_region /note="L2 repeat: matches 1666. .2008 of consensus"
20458. .20767
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20768. .20931
repeat_region /note="FRAM repeat: matches 0. .163 of consensus"
21050. .21545
repeat_region /note="Char11e1b repeat: matches 14. .523 of consensus"
21602. .21901
repeat_region /note="AluSg1 repeat: matches 1. .300 of consensus"
22056. .22620
repeat_region /note="LTR26 repeat: matches 43. .603 of consensus"
22624. .22930
repeat_region /note="Aluub repeat: matches 1. .311 of consensus"
22938. .23111
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23112. .23183
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24335. .24701
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25142. .25235
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27313. .27526
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31157. .31458
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32799. .33196
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33312. .33444
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34016. .34172
repeat_region /note="MER5A repeat: matches 32. .185 of consensus"
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35365. .35355
repeat_region /note="MER45 repeat: matches 1. .171 of consensus"
36270. .36567
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41820. .46785
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46786. .47086
repeat_region /note="Alu repeat: matches 3. .299 of consensus"
47087. .48267
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48774. .48803
repeat_region /note="L1MC repeat: matches 905. .934 of consensus"
49784. .49831
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50342. .50612
repeat_region /note="MER44 repeat: matches 421. .728 of consensus"
51509. .51638
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57676. .57908
repeat_region /note="L1MA8 repeat: matches 5986. .6242 of consensus"
57912. .58211
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58373. .58500
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58705. .59004
repeat_region /note="AluSx repeat: matches 1. .295 of consensus"
59121. .59259
repeat_region /note="MER33 repeat: matches 7. .149 of consensus"

Query Match 4.1%; Score 40.8; DB 9; Length 133021;
Best Local Similarity 49.5%; Pred. No. 2.2;
Matches 105; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 587 tcattacatacatgacaaatacatatgacccataattgttttggagcagagt 646
DB 12318 TCAGTTTCATTCATTTCTTAAGCTTAATTAATGAAGAGGCTTACGATTACGT 12377
QY 647 ggtgtgtccttttttttaccagaaatgcataatgcgcgcgcagatgcygcaatcsg 706
DB 12378 GAATTTCTTCTTTTCTTTTCTTTTGAATGACATTTTGTGTGAGGCTTATTACTG 12437
QY 707 atgacgctgcgagacagcagcaatcagacactacacacatgctttgtctgcggacaca 766
DB 12438 ATTATGCATFAGCAAGGAAATAGATTGTATATTATTCACCTTTTTCGTAAGCA 12497
QY 767 ataatagttttqtaacaaaataataactcta 798
DB 12498 ATAGAGGTTTCAGTGAGATTTTAAATAATTA 12529

RESULT 8
AC037428 142184 bp DNA linear HTG 26-MAY-2000
LOCUS Homo sapiens chromosome 12 clone Rpl1-631A22 map 12, WORKING DRAFT
DEFINITION
SEQUENCE, 18 unordered pieces.
AC037428
VERSION
AC037428.2 GI:8077012
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 142184)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 12, clone Rpl1-631A22
unpublished
2 (bases 1 to 142184)
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beta, F.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, T., Colangelo, M., Collins, S.,
Collins, R., Cooke, P., Develiano, K., Dewar, K., Diaz, J. S.,
Dodgson, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardina, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, C., Hago, B., Heaford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Laroque, K., Lamazares, R., Landers, T., Lehotzky, N.,
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Menus, L., Mihova, T., Miranda, C., Mlenka, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Olivari, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rotman, D.,

Qy 661 ttcttacacgaatgcacatagctgcccga 692
Db 63390 TTTTGTGTCACAAACAACATGCTGTCGCA 63421

RESULT 9
AP000736/c 81580 bp DNA linear PLN 27-DEC-2000
LOCUS Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K17E7.
DEFINITION AP000736 BA000014
ACCESSION AP000736.3 GI:8843906
KEYWORDS
SOURCE Arabidopsis thaliana (strain:Columbia) DNA, clone:lib:Mitsui TAC
clone:K17E7.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (sites)
AUTHORS Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
TITLE Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 pl, TAC
and BAC clones
JOURNAL DNA Res. 7 (3), 217-221 (2000)
MEDLINE 20363099
REFERENCE 2 (bases 1 to 81580)
AUTHORS Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-1999) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research, 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:yinakam@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
On Jun 29, 2000 this sequence version replaced gi:6451951.
COMMENT Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/sgd.graph.cgi?c=K17E7
'genes' with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://combio.ornl.gov/grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
Netemerk (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/Netemerk2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlin.zool.iastate.edu/cgi-bin/dsp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is T26G12 and the 3' clone is T20F20.

FEATURES
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/strain="Columbia"
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/chromosome="3"
/clone="K17E7"
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955. 5085
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polyprotein
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/evidence=not_experimental
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CDS
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DOKSQHVEAYMKMLERMSPEDKDPQDISGNSQSHRMKLSIDENKEIFPKLTID
KGNPFGISLVETLNKRRRRESYASSSTYAQLOEQOLKMSBDAEDNACDEHRO
SOSRLASLEKLVLTFRKDDPELDATLSDSDIVEVTLPTTHHSHNRHSPPTNHHRS
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TRLRLSLSDIDIKPSLNKRVAKMSPISDELRRYSRKATVY"
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/protein_id="BAB02993.1"
/db_xref="GI:13477080"
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EAEALAIATLQAKSLGFSFIPSSANGADLAKHALCAFESENSVPRHVKOKSYSG
VRSKQSGHTHPKSSSANGFL"
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/pseudo
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27647. .27820,28233. .28440,29579. .29743)
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/db_xref="GI:13477081"
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CRDLFVGEVEVCRDLFVGEVEGNNSSNLSFIRENNSSANLKYSSAKRFRV
EYSSAKRFRVETYSANLRVGENSSANLSPFGONLSSANLSFIRENNSSANLSS
FLAYVSQTCENIRKVCDDGIASMSCSGEETYSKRRVRETIYSKARRFGEIYSSA
NLRVGENNLSSANLSFIRENNLSSANLSIRKCVACRGTFPPAKPSQICDVAFAG
HMLANLEIYSSAKRFRVEIYSTRKRVGEIYSSANLRVGENSSANLSFIRENNSS
SANSIRISRRKCVAIYGGTFQPSQKRFATFGLGIMNSTQFPNCLANLGGKYLSS
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PVSQSSRNSSVAT"
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/note="contains similarity to non-ITR retroelement reverse
transcriptase
gene_id:K17E7.9"
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/pseudo
/evidence=not_experimental

[illegible]

DB	42606	TCAAACCAAATTAATAATTATTTTCACAAATAGCATGCAATTTTTGGTATTGCAAAACAAAAAAT	42547
OY	488	cgcagcagtcacatcgaggtggaacaagaactgaatacaaatc	534
Db	42546	TTGAATAGTCAGAACCAATTAATGACCAATTAATGAAATATCCACTTC	42500
RESULT	10		
AC027033/C			
LOCUS			
DEFINITION	Arabidopsis thaliana chromosome 1 BAC F21N10 genomic sequence,		
ACCESSION	AC027033	98017 bp	DNA linear PLN 11-OCT-2000
VERSION	AC027033		
KEYWORDS	Complete sequence.		
SOURCE	AC027033.3 GI:10092252		
ORGANISM	HTG. thale cress. Arabidopsis thaliana		
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 98017) Lin,X., Kaul,S., Town,C.D., Beitelo,M.-I., Creasy,T.H., Haas,B.J., Wu,D., Maitl,R., Ronning,C.M., Koob,H., Fujii,C.Y., Uteback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nieman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome I BAC F21N10 genomic sequence Unpublished 2 (bases 1 to 98017) Lin,X. and Kaul,S. Direct Submission Submitted (26-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 98017) Town,C.D. and Kaul,S. Direct Submission Submitted (12-SEP-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org On Sep 12, 2000 this sequence version replaced gi:7709919. Address all correspondence to:ateltgr.org		
COMMENT	BAC clone F21N10 is from Arabidopsis thaliana chromosome 1 The orientation of the sequence is from SP6 to T7 end of the BAC clone. Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CGC-081.mit.edu/GENSCAN.html), GenemarkHM (Mark Borodovsky, http://genemark.biology.gatech.edu/genemark/), Glimmer (a variant of GlimmerX, see Mihaela Pertea, http://www.tigr.org/software/glimmer.htm#glimmer.html , and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpeetel@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/cgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes with protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscans-SE/). Simple repeats are identified by repeatmasker (Arvan Smil, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Location/Qualifiers 1..98017 /organism="Arabidopsis thaliana" /cultivar="Columbia" /db_xref="taxon:3702" /chromosome="1" /clone="F21N10" 1184..5698 /gene="F21N10.12" /note="pseudogene, polypeptide" /pseudo		
FEATURES			
source			
gene			

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repeat_region      1407..1704
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repeat_region      3037..3529
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repeat_region      3037..3795
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                    ATCOP1A5 copia-like LTR-retrotransposon."
repeat_region      3124..3348
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                    ATCOP1A7 copia-like LTR-retrotransposon."
repeat_region      3407..3585
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                    ATCOP1A24 copia-like LTR-retrotransposon."
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                    ATCOP1A1 LTR-retrotransposon."
repeat_region      4256..4543
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                    ATCOP1A5 copia-like LTR-retrotransposon."
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                    ATCOP1A1 LTR-retrotransposon."
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                    ATCOP1A1 LTR-retrotransposon."
repeat_region      7115..7414
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repeat_region      7328..7416
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                    ARNOLD3."
repeat_region      9506..9634

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Query	Match	Best Local Similarity	Matches	Conservative	Score	DB	Length	Indels	Gaps
QY	368	tctggaatctactactcaactttttttaatggaagcaagttggaacacatgca	4.1%;	88;	40.6;	8;	98017;	0;	0;
Db	29557	TCGCAAACTAGTACTATTAAGCTTTTAAATATAAATAAAGCGAATCAAACTCAATGCA	52.7%;	0;	2.4;	79;	0;	0;	0;
QY	428	ttttcaaaagaagaatattatcttcaaacccacatgacatcaattctcaaacatgca	4.1%;	88;	40.6;	8;	98017;	0;	0;

QY	488	ccgacgagtcacatgcgaggctggaacgaagaacgtgaataacacac	534
Db	29437	TTGAAATAGTCAGAACCAAAATTTGAACCGAAATTAAGTAATTCACCTTC	293191
RESULT	11		
LOCUS	AC074329/c		
DEFINITION	Mus musculus chromosome 12 clone RP23-257D2 strain C57BL/6J,		
ACCESSION	AC074329	207872 bp	DNA linear
VERSION	AC074329		
KEYWORDS	complete sequence.		
SOURCE	AC074329.2 GI:13273356		
ORGANISM	HTG. house mouse. Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 207872)		
AUTHORS	Smith,D.R.		
TITLE	Genome Therapeutics Corporation Sequencing Center: Mouse Genome		
JOURNAL	Sequence Data		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 207872)		
TITLE	Smith,D.R.		
JOURNAL	Direct Submission Submitted (23-AUG-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA 3 (bases 1 to 207872)		
REFERENCE	Smith,D.R.		
AUTHORS	Direct Submission		
TITLE	Submitted (11-MAR-2001) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA On Mar 11, 2001 this sequence version replaced gi:9885988.		
COMMENT			
FEATURES	location/Qualifiers		
SOURCE	1..207872		
	/organism="Mus musculus"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/chromosome="12"		
	/clone="RP23-257D2"		
	/clone_11b="RC1-23"		
	/clone_11b="RC1-23"		
BASE COUNT	64130 a 40080 c 40327 g 63334 t	1 others	
ORIGIN			
Query Match	4.1%; Score 40.6; DB 10; Length 207872;		
Best Local Similarity	54.3%; Pred. No. 2.8;		
Matches	82; Conservative 0; Mismatches 69; Indels 0; Gaps 0;		
QY	309	tgaacacccatgtatgtcatcagcgcctgatggaggaagcaacatgcacctttccct	368
Db	107309	TAAAGAAAATATGATGCCACAACCTACCACATCTATGCGACAAATGAAAGCATTTTCTATG	107250
QY	369	ctggaatcattagctcacacattttttaaagtgaagcaagatgtygcaaacatgcat	428
Db	107249	AGGAAACACTCATAGCTCAGAGAGTCTTCAAAAAAGAACTAGAGAAACACACACTAGCAG	107190
QY	429	tttcaacaaggaaataatctcaacaa	459
Db	107189	CTTGACAAATATACCTTAAAGCTCTGGAACAA	107159
RESULT	12		
LOCUS	AP003681/c		
DEFINITION	Oryza sativa genomic DNA, chromosome 1, BAC clone:B1158C05,		
ACCESSION	AP003681	65955 bp	DNA linear
VERSION	AP003681.2		
KEYWORDS	complete sequence.		
	HTG.		

[illegible]

Search completed: September 12, 2002, 07:27:09
Job time: 20617 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 04:57:23 : Search time 406.92 Seconds
(without alignments)
4219.292 Million cell updates/sec

Title: US-09-508-377-10_COPY_1_1000
Perfect score: 1000
Sequence: 1 agaacaccctcatttaga.....acactccccgtgggtccct 1000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*

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22:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1000	100.0	11473	20	AAK34650
2	1000	100.0	11475	22	AAH78338
3	39.4	3.9	4590	22	AAH24065
4	36	3.6	15548	24	ABL34155
5	35.6	3.6	1741	18	AAH84300
6	35.6	3.6	1741	19	AAV52578
7	35.2	3.5	8387	24	ABL32247
8	34.6	3.5	710	22	AAI97878
9	34.6	3.5	32220	22	AAI37568

10	34.4	3.4	362	22	AAK57698	Human immune/haema
11	34.4	3.4	9725	24	ABL33293	Human immune syste
12	34.4	3.4	20394	22	AAE24892	Human immune syste
13	34.2	3.4	6754	24	AAH61304	Human gene regulat
14	34.2	3.4	12767	22	ABH17068	Human nervous syst
15	34.2	3.4	101786	21	AAE22293	BAC containing rep
16	34.2	3.4	350	16	AAO99380	Rat allograft infl
17	34	3.4	350	16	AAO99380	Rat allograft infl
18	34	3.4	1279	23	AAH65600	Drosophila melanog
19	34	3.4	3640	23	ABL07702	Drosophila melanog
20	34	3.4	5340	22	AAE26289	P. falciparum egf
21	34	3.4	7810	22	AAH45434	Chemically pretrea
22	34	3.4	56153	22	AAH46794	Tumour suppressor
23	33.8	3.4	6183	24	ABL3196	Human immune syste
24	33.8	3.4	6415	22	AAH46371	Tumour suppressor
25	33.6	3.4	4590	22	AAH24065	Yeast AOD9604-asso
26	33.4	3.3	628	21	AAH40041	Arabidopsis thalia
27	33.4	3.3	2324	22	AAH16057	Human cDNA sequenc
28	33.2	3.3	1000	21	AAH02484	Human colon cancer
29	33.2	3.3	5886	24	ABL34212	Human immune syste
30	33.2	3.3	11812	22	AAH45501	Chemically pretrea
31	33.2	3.3	11812	22	AAH46741	Tumour suppressor
32	33.2	3.3	11812	24	ABL34118	Human immune syste
33	33.2	3.3	16771	22	AAH76778	Human immune/haema
34	33.2	3.3	17763	23	ABL02400	Drosophila melanog
35	33.2	3.3	168575	22	AAH21613	Human hypococtrin r
36	33	3.3	495	21	AAH36252	Arabidopsis thalia
37	33	3.3	6297	24	ABL32995	Human immune syste
38	33	3.3	15923	24	AAH61132	Human gene regulat
39	33	3.3	32176	22	AAH36453	Human cardiovascular
40	33	3.3	32178	22	AAH36454	Human cardiovascular
41	32.8	3.3	347	22	AAH70921	Human immune/haema
42	32.8	3.3	347	22	AAH70922	Human immune/haema
43	32.8	3.3	700	22	AAH24329	Human breast cance
44	32.8	3.3	4329	22	AAH30492	DNA encoding novel
45	32.8	3.3	4329	22	AAH06272	Human reproductive

ALIGNMENTS

RESULT	ID	AAK34650 standard; DNA: 11473 BP.
AAK34650		
AC AAK34650;		
XX		
05-JUL-1999 (first entry)		
XX		
DE Starch branching enzyme II (SBE II) gene sequence.		
XX		
XX Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBS;		
KW starch branching enzyme; starch soluble synthase; debranching enzyme;		
KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;		
KW grain softness protein I; bacterial isomylase; glycogen synthase;		
KW WBE I-D4 gene; ss.		
XX		
OS Trifolium tauschii.		
XX		
PN WO9914314-A1.		
XX		
PD 25-MAR-1999.		
XX		
PF 11-SEP-1998; 98WO-AU00743.		
XX		
PR 20-MAR-1998; 98AU-0002509.		
XX		
PR 12-SEP-1997; 97AU-0009108.		
XX		
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.		
PA (GOOD-) GOODMAN FIELDER LTD.		
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.		
PA (AUSU) UNIV AUSTRALIAN NAT.		
XX		

06-NOV-2000; 2000MO-AU01362.
05-NOV-1999; 99AU-0003875.
(META-) METABOLIC PHARM LTD.
Belyea CI, Ng FM, Vaughan P;
WPI: 2001-328876/34.
New organisms containing nucleic acid encoding a growth hormone
fragment which modulates lipid metabolism are useful to produce dietary
aids for obesity and in the meat production industry -
Disclosure: Page 48-50; 54pp; English.
The invention relates to novel transgenic organisms useful in the
production of functional food and drink products for the treatment
or prevention of obesity via the regulation of lipid metabolism. The
organisms comprise a polynucleotide encoding a growth hormone fragment
capable of stimulating the activity of hormone-sensitive lipase (the key
enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key
enzyme in lipogenesis). The growth hormone fragment preferably contains
at least the disulphide-bonded loop of a mammalian growth hormone (but is
not the full-length growth hormone) and is optionally linked to an
epitope tag or heterologous fusion protein partner. The transgenic
organism may be a microorganism used to produce a fermented product
(e.g., yeast), or an edible plant or animal or cell thereof. Food or
drink made using methods of the invention are used to modify fat/lean
ratio, lipid metabolism or food use in a mammal. In particular, the food
or drink products may be used to treat or prevent obesity, particularly
in humans, and may also be used to improve the fat/lean ration of
livestock raised for meat production. In the exemplification of the
invention, the human growth hormone (hGH) fragment analogue AOD9604 was
expressed in yeast, optionally fused to the FLAG epitope (AAB33625).
The present sequence is described as a DNA sequence from yeast in
the sequence listing, but is not further referred to in the
specification.

Query Match	Similarity	Score	DB	Length
Best Local	9.08	Pred. No. 0.21		
Matches	48	Conservative	252	Mismatches 234; Indels 0; Gaps 0
OY	257	cgtcacacatggtgatcatcatatcggtgcgtgcgacgaagagagacgacatgaacac	316	
Db	3585	msaandrwngsdactbhsntrdaideagyscmrgmatthdaayntrmtmthandyaag	3644	
OY	317	atgatgatgctatcagcgctgatgagaggagaacacatgacccctttccctctggaat	376	
Db	3645	cbbrmrgmatnrvbmrntiraansmnoasnmrgmatydaarsachandvymnc	3704	
OY	377	tcatagctcacactttttttatggaagcagaggttgccaacacatgatttcaaac	436	
Db	3705	tlaandramtnvstyaethrtyradsaarchanandstirdvmttbythraentattn	3764	
OY	437	aaggaataatlaattctcaaacacacatgacatgcaattctcaaacatgacccgaaggt	496	
Db	3765	ysgrthackwksnsttatntandtradmarrkatrnysastraaagagammrgm	3824	
OY	457	ccatcgcgaggttgaaacgaagaacatgaaatacaacatccacagtgtcgagtcgagaag	556	
Db	3825	atmbshmwmdyskdcumdmmykcdakcdmtnqhyhnmrbpddhdndrdwvbwhtc	3884	
OY	557	gatgcacgaagaatcatgtaatcgattcatcatatcacatgcaacaataacaatg	616	
Db	3885	dwbhnhwddhdhdhdhdhdhndwchmnbvhdhdhdddyymrgmnhnnhnhnt	3944	
OY	617	taacctacaattgttttttgagcagagtggtgtgtcttttttttacaagaaatg	676	
Db	3945	cchddhnhntchadgmnnvvvvvvvvvvvvvchkhhdhghmmcmhccmklmch	4004	

[illegible]

RESULT	4
ABL34155/c	
ID	ABL34155 standard; DNA; 15548 BP.

AC ABL34155;

DT 26-MAR-2002 (first entry)

DE Human immune system associated gene SEQ ID NO: 2128.

Human; immune system disease; cytosine methylation; antiasthmatic; KW

KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

KW antiinflammatory; cancer; eye disease; arteriosclerosis; ana

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

[illegible]

XX

XX

XX 7

XX

PR 01-SEP-2000; 2000DE-1043826.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-130909/17.

PT Nucleic acid comprising fragment of chemically modified gene, useful

PT cytosine methylation -

PS Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German.

CC The present invention provides a number of human immune system associated

CC can be used in the diagnosis and treatment of immune system disorders,

CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

CC rheumatoid arthritis, psoriasis and inflammatory bowel

XX

Query Match 3.68; Score 36; DB 24; Length 15548;

Matches	93;	Conservative	0;	Mismatches	95;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	-----	--------	----	------	----

427 atttcaacaagaaatlaattctcaaacccatgacatgcaattctcaaacctgc 486

Db 7849 ATCTAAATCAACTTAAAAAATTATTTTTACCAAATTAATAATACATTTCATTAACACAAC 7790

QY 487 accgacgagtcctcgtcgaggtggaacgagaactgaaatcaacatccagttgtcgag 546

```
DB 7789 CTTAAAAAACTTACACATATACCCAAATATCAAAATCTTACTTTATACAT 7730
QY 547 tcgagaagagatgacactgaagatgctgatacattcatatcacatgacaa 606
DB 7729 TTTAAAAAAACATATCATATACATCTTAAATATACATTTATATTCGATCTTAA 7670
QY 607 atacataa 614
DB 7669 AAACAAAA 7662
```

RESULT 5

```
AAAT84300
ID AAT84300 standard; cDNA; 1741 BP.
XX
AC AAT84300;
XX
DT 10-NOV-1997 (first entry)
XX
DE Quail Flt4 receptor tyrosine kinase ligand VEGF-C cDNA.
XX
KW VEGF-C; Flt4; receptor tyrosine kinase; VEGFR-3; quail;
KM vascular endothelial growth factor receptor-3; ligand;
XX angiogenesis; wound healing; lymph vessel; therapy; diagnosis; ss.
OS Coturnix coturnix.
```

```
XX
FH Key Location/Qualifiers
FT CDS 453..1709
FT /tag= a
XX
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WO9705250-A2.

13-FEB-1997.

01-AUG-1996; 96WO-F100427.

28-JUN-1996; 96US-0671573.

01-AUG-1995; 95US-0510133.

12-JAN-1996; 96US-0585895.

14-FEB-1996; 96US-0601132.

(UYHE-) UNIV HELSINKI LICENSING LTD OY.

Alitalo K, Joukov V;

WPI; 1997-145688/13.

P-PSDB; AAM00934.

Example 20; Page 124-126; 183pp; English.

This cDNA clone codes for quail VEGF-C (AAM00934), a novel ligand that binds specifically to the Flt4 receptor tyrosine kinase (VEGFR-3), stimulating phosphorylation of the receptor. The clone was isolated from a quail cDNA library using mouse (see AAT84277) CC and human (see AAT84276) VEGF-C cDNA fragments as probes. The CC isolated polynucleotide can be used to produce recombinant CC polypeptides corresponding to non-human mammalian variants of VEGF-C.

Sequence 1741 BP; 445 A; 455 C; 449 G; 392 T; 0 other;

```
DB 41 cggcccgaggagggcgcgctgcagcgccactgggctcctcctcctccccc 100
QY 885 agcgtccctccacgcgtccctcgtcgtccacccctcgtgctgcgcgcgaaggga 944
DB 101 tctcctcctccctcctcctcctcgtcgtccacgcgtcccgagcgacgctcgga 160
QY 945 gg 946
DB 161 tg 162
```

RESULT 6

```
AAV52578
ID AAV52578 standard; cDNA; 1741 BP.
XX
AC AAV52578;
XX
DT 14-DEC-1998 (first entry)
XX
DE Quail vascular endothelial growth factor C gene.
XX
KW Flt4; vascular endothelial growth factor C; vascular endothelial cell;
KM lymphatic endothelial cell; myelopoiesis; angiogenesis; inflammation;
XX lymphangiogenesis; oedema; elephantiasis; Milroy's disease; ss.
OS Coturnix sp.
```

```
XX
FH Key Location/Qualifiers
FT CDS 453..1709
FT /tag= a
FT /product= "VEGF-C"
XX
```

WO9833917-A1.

06-AUG-1998.

02-FEB-1998; 98WO-US01973.

05-FEB-1997; 97US-0795430.

(LUDW-) LUDWIG INST CANCER RES.

(UYHE-) UNIV HELSINKI LICENSING LTD.

Alitalo K, Joukov V;

WPI; 1998-437470/37.

P-PSDB; AAM75743.

New isolated vascular endothelial growth factor polypeptide(s) - used to develop products for treating, e.g. cancers, inflammation, PT oedema, granulocytopenia or for wound healing or tissue transplantation

Example 20; Page 121-123; 177pp; English.

The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells, CC promoting growth of lymphatic endothelial cells and lymphatic vessels, CC increasing vascular permeability, and affecting myelopoiesis. The CC products can be used for stimulating angiogenesis, for inhibiting CC angiogenesis, for stimulating lymphangiogenesis, treatment or prevention CC of inflammation, oedema, elephantiasis, or Milroy's disease. They can CC also be used to modulate myelopoiesis, e.g. treating granulocytopenia. CC They can also be used for modulating the growth of endothelial cells. CC and to promote or inhibit trafficking of leucocytes between tissues and CC lymphatic vessels or to affect migration in and out of the thymus.

Sequence 1741 BP; 445 A; 455 C; 449 G; 392 T; 0 other;

Query Match 3.6%; Score 35.6; DB 18; Length 1741;
Best Local Similarity 55.7%; Pred. No. 1.9; Mismatches 0; Gaps 0;
Matches 68; Conservative 0; Indels 54; Indels 0; Gaps 0;

QY 825 cggcatgagccagtgtaacgagcgtcccgctgtgttgatcgtctcctccgcacgc 884

Query Match 3.6%; Score 35.6; DB 19; Length 1741;

Db 329 ATCAGAGCTTTCACCCAGGCTTTATAGCAAAAAAACAATAACCAACCTTAG 270
Oy 464 gacatgcattctcaaacatgacgcagagtcacatgagtggaacgaactga 523
Db 269 GACTTCATCTACTAGCCCTGACCTTGACAGTCCTCTGAGGGCCCTCTAAGACCCTT 210
Oy 524 aaatcacatcccggtgtgcagtcgagagagatgacactgaactga 572
Db 209 AAAATAATTATACATAGGACTTGTGATTCATTTCACAGTGAAATA 161

RESULT 9
ID AAL37568 standard; DNA: 32220 BP.
XX AAL37568;
XX AAL37568;
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3933.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW candidant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.
XX
OS Homo sapiens.
XX
PN WO200155367-A1.
XX
PD 02-AUG-2001.
XX
PE 17-JAN-2001; 2001WO-US01338.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 25-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236357.
PR 29-SEP-2000; 2000US-0236358.
PR 29-SEP-2000; 2000US-0236359.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249211.

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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
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PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233297.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
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PR 21-SEP-2000; 2000US-0234223.
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PR 17-NOV-2000; 2000US-0249264.
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PR 17-NOV-2000; 2000US-0249297.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
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PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-483426/52.
DR P-PSDB; AAM84917.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Claim 1: SEQ ID NO 2758; 3071pp + Sequence Listing: English.
XX
XX AAK4951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 362 BP; 89 A; 80 C; 85 G; 106 T; 2 other;

Query Match 3.4%; Score 34.4; DB 22; Length 362;
Best Local Similarity 57.4%; Pred. No. 1.9; Mismatches 46; Indels 0; Gaps 0;
Matches 62; Conservative 0;

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II IIIIIII III III III III III III III III III II
Db 243 tatagttttttaacttaactaataattttcacaagtcctagagcctaagaatcc 302
II IIIIIII III III III III III III III III III II
QY 828 catgcccaggtaaagcgcgtccagcgcgtgtgttcgcatcgtctcc 875
I IIIII III III III III III III III III III III II
Db 303 aagatcaagtgccagcagcagcgtcagtttgytaagaggtctcttct 350
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XX
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Job time: 12219 sec

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 QY 837 gtaacg 843
 Db 1501 aaaaacg 1507

RESULT 15

AAE22293/C
 ID AAF22293 standard; DNA; 101786 BP.

AC AAF22293;

DT 20-MAR-2001 (first entry)

DE BAC containing repeats from centromeres 1-4 #16.

KW Centromere; microsome; vector; ds.

OS Arabidopsis thaliana.

PN WO200055325-A2.

PD 21-SEP-2000.

PF 17-MAR-2000; 2000WO-US07392.

PR 18-MAR-1999; 99US-0125219.

PR 01-APR-1999; 99US-0127409.

PR 18-MAY-1999; 99US-0134770.

PR 13-SEP-1999; 99US-0153584.

PR 17-SEP-1999; 99US-0154603.

PA (UYCH-) UNIV CHICAGO.

PI Preuss D, Copenhaver G, Keith K;

DR WPI: 2000-587529/55.

PS Claim 102; Page 626-650; 1449pp; English.

CC The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited microsome which can serve as vectors for the construction of transgenic plant and animal cells

CC selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.

CC Sequence 101786 BP; 31952 A; 18054 C; 19869 G; 31909 T; 2 other;

Query Match 3.4%; Score 34.2; DB 21; length 101786;
 Best Local Similarity 58.3%; Pred. No. 60;
 Matches 60; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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 Db 53563 TGAACCTAAACCTAGTCTAATGTAATCAAGAACTTCGCAACACGCCAAT 53504

QY 430 ttcaacaaggaataattctcaaacacacatgacatgcaa 472
 Db 53503 TTGATATAAGTTAATTATCTAAGACCACTCTCAATAATA 53461

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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2647.198 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/lna/PCITUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	39.8	4.0	7218	1	US-08-232-463-14
C 2	35.6	3.6	1741	3	US-08-795-430-12
C 3	34	3.4	350	1	US-08-171-385-14
C 4	34	3.4	350	3	US-08-361-441B-14
C 5	32.6	3.3	15144	4	US-08-458-434A-6
C 6	32.2	3.2	1208	4	US-08-979-608A-16
C 7	31.8	3.2	35060	3	US-08-814-095-7
C 8	31.2	3.1	726	4	US-08-998-416-1085
C 9	31.2	3.1	1767	1	US-08-399-646-1
C 10	31.2	3.1	1767	1	US-08-607-321-1
C 11	31.2	3.1	1767	2	US-08-961-240-1
C 12	31.2	3.1	1767	2	US-08-605-501-1
C 13	31.2	3.1	2161	1	US-08-399-646-11
C 14	31.2	3.1	2161	1	US-08-607-321-11
C 15	31.2	3.1	2161	2	US-08-961-240-11
C 16	31.2	3.1	2161	2	US-08-605-501-11
C 17	30.8	3.1	3284	6	5258288-3
C 18	30.6	3.1	19124	2	US-08-487-826B-13
C 19	30.4	3.0	4252	2	US-08-475-844-4
C 20	30.4	3.0	4252	5	PCT-US95-08429-4
C 21	30.2	3.0	1623	4	US-08-339-214-25
C 22	30.2	3.0	7791	2	US-08-149-097D-23
C 23	30.2	3.0	7791	3	US-08-949-386-23
C 24	30.2	3.0	7791	3	US-08-450-562-23
C 25	30.2	3.0	7791	4	US-08-984-709A-23
C 26	30.2	3.0	7808	2	US-08-149-097D-22
C 27	30.2	3.0	7808	3	US-08-949-386-22

C 28	30.2	3.0	7808	3	US-08-450-562-22	Sequence 22, Appl
C 29	30.2	3.0	7808	4	US-08-984-709A-22	Sequence 22, Appl
C 30	30	3.0	3719	1	US-08-920-812-10	Sequence 10, Appl
C 31	30	3.0	3719	1	US-08-920-812-10	Sequence 10, Appl
C 32	30	3.0	3719	1	US-08-921-177-10	Sequence 10, Appl
C 33	30	3.0	3719	1	US-08-362-577C-10	Sequence 10, Appl
C 34	30	3.0	3719	2	US-08-920-828-10	Sequence 10, Appl
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C 37	29.8	3.0	7676	2	US-08-998-208-7	Sequence 7, Appl
C 38	29.8	3.0	7676	5	PCT-US95-06743-7	Sequence 7, Appl
C 39	29.4	2.9	976	1	US-08-125-628-7	Sequence 7, Appl
C 40	29.4	2.9	29598	4	US-09-341-587-6	Sequence 6, Appl
C 41	29.2	2.9	340	1	US-08-171-385-27	Sequence 27, Appl
C 42	29.2	2.9	340	1	US-08-361-441B-27	Sequence 27, Appl
C 43	29.2	2.9	3396	4	US-08-974-549A-640	Sequence 640, Appl
C 44	29.2	2.9	40352	3	US-08-846-111D-15	Sequence 15, Appl
C 45	29	2.9	1678	1	US-08-261-677-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-F1s
US-08-232-463-14

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2
US-08-795-430-12
Sequence 12, Application US/08795430
Patent No. 6130071
GENERAL INFORMATION:
APPLICANT: Alltalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133

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1      FILLING DATE: 01-ANG-1995
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3      PRIOR APPLICATION DATA:
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5      APPLICATION NUMBER: 08/340,011
6
7      FILLING DATE: 14-NOV-1994
8
9      ATTORNEY/AGENT INFORMATION:
10
11      NAME: Gass, David A.
12
13      REGISTRATION NUMBER: 38,153
14
15      REFERENCE/DOCKET NUMBER: 28967/33691
16
17      TELECOMMUNICATION INFORMATION:
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19      TELEPHONE: 312/474-6300
20
21      TELEFAX: 312/474-0448
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23      TELE: 25-3856
24
25      INFORMATION FOR SEQ ID NO: 12:
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27      SEQUENCE CHARACTERISTICS:
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29      LENGTH: 1741 base pairs
30
31      TYPE: nucleic acid
32
33      STRANDEDNESS: single
34
35      TOPOLOGY: linear
36
37      MOLECULE TYPE: cDNA
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39      FEATURE:
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41      NAME/KEY: CDS
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43      LOCATION: 453..1706
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Oy	945	ggg	946		
Db	161	tg	162		

RESULT 3
 ; Sequence 14, Application US/08171385
 ; Patent No. 3527864
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary E. Russell
 ; APPLICANT: Ullive Utans
 ; TITLE OF INVENTION: Mediators of Chronic Allograft
 ; TITLE OF INVENTION: Rejection
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/171.385
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fraser, Janis K.

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1      REGISTRATION NUMBER: 34,4819
2      REFERENCE/DOCKET NUMBER: 05433/0060001
3      TELECOMMUNICATION INFORMATION:
4      TELEPHONE: (617) 542-5070
5      TELEFAX: (617) 542-6906
6      TELEX: 200154
7      INFORMATION FOR SEQ ID NO: 14:
8      SEQUENCE CHARACTERISTICS:
9          LENGTH: 350
10         TYPE: nucleic acid
11         STRANDEDNESS: double
12         TOPOLOGY: linear
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14 US-08-171-385-14

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QY	681	agctgcccgcgaatgcgtaacatcgtatcgtctggagagcgcgacacatcagacact	740
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QY	801	aa 802	
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RESULT 4
 Sequence 14, Application US/08361441B
 Patent No. 6077948
 GENERAL INFORMATION:
 APPLICANT: Russell, Mary E.
 APPLICANT: Utans, Ulrike
 TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08361,441B
 FILING DATE: 21-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/171,385
 FILING DATE: 21-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 05433/014001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070

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? TELEFAX: 617/542-8906
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? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 350 base pairs
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? TYPE: nucleic acid
?
? STRANDEDNESS: double
?
? TOPOLOGY: linear
?
US-08-361-441B-14

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Best Local Similarity	46.3%	Pred. No	0.27	
Matches 112	Conservative	0	Mismatches 130	Indels 0
				Gaps 0

Qy	561	aacacgaagatgctgcttccagcttccatctaacatcgttcaacaaatacatatgacc	620
Db	246	ACACTTATACCCACAGATTTTACATAGCCATATACATGTATGTTTACATTAACATTAAAGG	187
Qy	621	ctacaatttgttttttggagcagagtggtgtgctcttttttcaacgaaatgcat	680
Db	186	TTAGATTTATATATATTAAGAAAGAACATGTGGTGTTCTTATTCGAGTCGGATTAATTTT	127
Qy	681	agctggccgcgacgctgacagatcggatgcgltcggagacgagcaatcagacac	740
Db	126	GCTCATATATATAATATTCACATCCATCCATCAATTTTCCATTAAGTTTATATATTTTCATTAT	67
Qy	741	cacacagcttctgtctcggacacaataatgttttctgaacaaataataactata	800
Db	66	GGCTTAATTAATAATCTGTGTGTATGTAAAAAATAAAAAAAAAAAAAAAAAAAAAA	7

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LENGTH: 15144 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-458-434A-6

Query Match
Best Local Similarity 3.3%; Score 32.6; DB 3; Length 15144;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 466 catgcacattccaaacatgacaccgagtgccatgaggtggaacgaagactgaa 525
DB 11759 CAAGCACTTGTCTCAGACGCTTCATGTAGACTTTGCATCTTAATACACAACTGAAA 11700
QY 526 atcaaatcccatgtgtcgagtcgagaagagagatgacactgaaagtatcgcttaacgat 585
DB 11699 AACAACTACAAATTCCTTTTGGAAATTTATATACAAACCCGATATTCTTCGTGAT 11640

QY 586 ttcatatcatatgatacaaat 608
DB 11639 TACATATTAATACATTAATACTAT 11617

RESULT 6
US-08-979-608A-16
Sequence 16, Application US/08979608A
Patent No. 6355451

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.

Arjona, Anibal A.
Law, Simon W.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND

TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

STATE: MA
COUNTRY: USA

ZIP: 02110-2804
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A

FILING DATE: 26-NOV-1997
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis

REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1...651
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-979-608A-16

Query Match
Best Local Similarity 3.2%; Score 32.2; DB 4; Length 1208;
Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 197 gaaagacgtcgaagcagagagccacacacagcttgagccctgacagcggagctgagtg 256
DB 93 GAATGACCGCTGCGAGGTGCCGACGACCAACGACTTAACGGCGAGCGGAGCTCAGAG 152

QY 257 cgtgacacatggggtca 273
DB 153 TGCCAGAGGAGGGGTCA 169

RESULT 7
US-08-814-095-7
Sequence 7, Application US/08814095
Patent No. 6025183

GENERAL INFORMATION:
APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: KOHN & ASSOCIATES

STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills

STATE: Michigan
COUNTRY: U.S.

ZIP: 48334
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095

FILING DATE:
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.

REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066

TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs

TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Cosmid including ACHÉ
DESCRIPTION: promoter, ACHÉ gene and ARS gene"

HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Homo sapiens

POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22

FEATURE:
NAME/KEY: promoter

LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHÉ Promotor"

OTHER INFORMATION: /standard_name= "ACHÉ Promotor"

FEATURE:

1	NAME/KEY:	exon	
2	LOCATION:	22465..22537	
3	OTHER INFORMATION:	/function= "non-translated"	
4	OTHER INFORMATION:	/gene= "ACHE"	
5	OTHER INFORMATION:	/number= 1	
6	FEATURE:		
7	NAME/KEY:	exon	
8	LOCATION:	24090..25177	
9	IDENTIFICATION METHOD:	experimental	
10	OTHER INFORMATION:	/function= "(translation start:"	
11	OTHER INFORMATION:	/function= "4110)"	
12	OTHER INFORMATION:	/evidence= EXPERIMENTAL	
13	OTHER INFORMATION:	/gene= "ACHE"	
14	OTHER INFORMATION:	/number= 2	
15	FEATURE:		
16	NAME/KEY:	exon	
17	LOCATION:	25524..26009	
18	IDENTIFICATION METHOD:	experimental	
19	OTHER INFORMATION:	/evidence= EXPERIMENTAL	
20	OTHER INFORMATION:	/gene= "ACHE"	
21	OTHER INFORMATION:	/number= 3	
22	FEATURE:		
23	NAME/KEY:	exon	
24	LOCATION:	27005..27274	
25	IDENTIFICATION METHOD:	experimental	
26	OTHER INFORMATION:	/evidence= EXPERIMENTAL	
27	OTHER INFORMATION:	/gene= "ACHE"	
28	OTHER INFORMATION:	/number= 4	
29	FEATURE:		
30	NAME/KEY:	exon	
31	LOCATION:	27255..28007	
32	IDENTIFICATION METHOD:	experimental	
33	OTHER INFORMATION:	/evidence= EXPERIMENTAL	
34	OTHER INFORMATION:	/gene= "ACHE"	
35	OTHER INFORMATION:	/number= 5	
36	FEATURE:		
37	NAME/KEY:	terminator	
38	LOCATION:	27385..27387	
39	FEATURE:		
40	NAME/KEY:	exon	
41	LOCATION:	28008..28129	
42	IDENTIFICATION METHOD:	experimental	
43	OTHER INFORMATION:	/evidence= EXPERIMENTAL	
44	OTHER INFORMATION:	/gene= "ACHE"	
45	OTHER INFORMATION:	/number= 6	
46	FEATURE:		
47	NAME/KEY:	terminator	
48	LOCATION:	28129..28131	
49	FEATURE:		
50	NAME/KEY:	exon	
51	LOCATION:	complement (34528..34895)	
52	OTHER INFORMATION:	/function= "arsenite resistance"	
53	OTHER INFORMATION:	gene=	
54	OTHER INFORMATION:	/gene= "AR"	
55	OTHER INFORMATION:	/number= 1	
56	FEATURE:		
57	NAME/KEY:	exon	
58	LOCATION:	complement (34092..34358)	
59	OTHER INFORMATION:	/gene= "AR"	
60	OTHER INFORMATION:	/number= 2	
61	FEATURE:		
62	NAME/KEY:	exon	
63	LOCATION:	complement (33779..33963)	
64	OTHER INFORMATION:	/gene= "AR"	
65	OTHER INFORMATION:	/number= 3	
66	FEATURE:		
67	NAME/KEY:	exon	
68	LOCATION:	complement (33493..33591)	
69	OTHER INFORMATION:	/gene= "AR"	
70	OTHER INFORMATION:	/number= 4	
71	FEATURE:		
72	NAME/KEY:	exon	
73	LOCATION:	complement (33297..33408)	

[illegible]

;; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
;; NUMBER OF SEQUENCES: 18
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/605,501
;; FILING DATE: 26-FEB-1996
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/399,646
;; FILING DATE: 07-MAR-1995
;; APPLICATION NUMBER: JP 59834
;; FILING DATE: 07-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 59840
;; FILING DATE: 07-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: KUBOTA-5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;;
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1767 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..1767
;; US-08-605-501-1

Query Match 3.1%; Score 31.2; DB 2; Length 1767;
Best Local Similarity 54.3%; Pred. No. 5.8;
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 820 gctaacgcatgcccgaagcgcctccagcgcgttggttgcatctgtctcccg 879
DB 1357 gccacgcccgcagagcagatcagagaggttcgacgcgcatgggggtggatcccgccgctg 1416

QY 880 caacgcagctgcctccacgcgtcgcgtgcgtgcacacctgtgctgcgcgc 935
DB 1417 cccgattcccgagatccgagaccttcaccccgctccaaactggactggcggaagc 1472

RESULT 13
US-08-399-646-11
; Sequence 11, Application US/08399646
; Patent No. 5556781
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/399,646
;; FILING DATE: 07-MAR-1995
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 59834
;; FILING DATE: 07-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 59840
;; FILING DATE: 07-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: KUBOTA-5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;;
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2161 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 207..1994
;; US-08-399-646-11

Query Match 3.1%; Score 31.2; DB 1; Length 2161;
Best Local Similarity 54.3%; Pred. No. 6.6;
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 820 gctaacgcatgcccgaagcgcctccagcgcgttggttgcatctgtctcccg 879
DB 1584 gccacgcccgcagagcagatcagagaggttcgacgcgcatgggggtggatcccgccgctg 1643

QY 880 caacgcagctgcctccacgcgtcgcgtgcgtgcacacctgtgctgcgcgc 935
DB 1644 cccgattcccgagatccgagaccttcaccccgctccaaactggactggcggaagc 1699

RESULT 14
US-08-607-321-11
; Sequence 11, Application US/08607321
; Patent No. 5716813
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA


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;
;   ZIP: 20004
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/607,321
;   FILING DATE: 26-FEB-1996
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/399,646
;   FILING DATE: 07-MAR-1995
;   APPLICATION NUMBER: JP 59834
;   FILING DATE: 07-MAR-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 59840
;   FILING DATE: 07-MAR-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: BROWDY, Roger L.
;   REGISTRATION NUMBER: 25,618
;   REFERENCE/DOCKET NUMBER: KUBOTA-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-628-5197
;   TELEFAX: 202-737-3528
;   TELEX: 248633
;   INFORMATION FOR SEQ. ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2161 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 207..1994
;
US-08-607-321-11

Query Match          3.1%; Score 31.2; DB 1; Length 2161;
Best Local Similarity 54.3%; Pred. No. 6.6;
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 820 gctaacgcatgcccaggtataacgcgtcccaacgctgtgttgcgattcgcgtcccg 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1584 GCCACGCCGCGACGAGATCAGGAGCTTCGACGCGATGGGTGGATCCCGCGTGTG 1643
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 880 cagcagcgctgcctccacgcgtcgcgtcgcgtccacactcgtgtgcgcgcgc 935
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1644 CCCGATCCGCGAGATCCGAGACCTTCACCCGCTCCAACTGACTGGCGGGAAGC 1699

RESULT 15
US-08-961-240-11
; Sequence 11, Application US/08961240
; Patent No. 5830715
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/961,240
;   FILING DATE: 30-OCT-1997
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/399,646
;   FILING DATE: 07-MAR-1995
;   APPLICATION NUMBER: JP 59834
;   FILING DATE: 07-MAR-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 59840
;   FILING DATE: 07-MAR-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: BROWDY, Roger L.
;   REGISTRATION NUMBER: 25,618
;   REFERENCE/DOCKET NUMBER: KUBOTA-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-628-5197
;   TELEFAX: 202-737-3528
;   TELEX: 248633
;   INFORMATION FOR SEQ. ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2161 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 207..1994
;
US-08-961-240-11

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Query Match          3.1%; Score 31.2; DB 2; Length 2161;
Best Local Similarity 54.3%; Pred. No. 6.6;
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 820 gctaacgcatgcccaggtataacgcgtcccaacgctgtgttgcgattcgcgtcccg 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1584 GCCACGCCGCGACGAGATCAGGAGCTTCGACGCGATGGGTGGATCCCGCGTGTG 1643
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 880 cagcagcgctgcctccacgcgtcgcgtcgcgtccacactcgtgtgcgcgcgc 935
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1644 CCCGATCCGCGAGATCCGAGACCTTCACCCGCTCCAACTGACTGGCGGGAAGC 1699

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Search completed: September 12, 2002, 08:12:27
 Job time: 14804 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 03:32:50 : Search time 3207.55 Seconds
(without alignments)
4207.871 Million cell updates/sec

Title: US-09-508-377-10_COPY_1_1000
Perfect score: 1000
Sequence: 1 agaaccacctcatcttaga.....acatcccccgtggtccct 1000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estda: *
2: em_esthum: *
3: em_estin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_estl: *
10: gb_estl2: *
11: gb_hlc: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_iny: *
15: em_gss_pln: *
16: em_gss_vtl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47.6	4.8	1101	12	CNS00LT2
2	47.7	4.7	1101	9	AL513871
3	43.4	4.3	844	12	CNS0052P
4	40.4	4.0	931	10	BF142642
5	38.6	3.9	427	10	BG895352
6	38.6	3.9	1031	10	W29451
7	38.4	3.8	866	10	BI953458
8	38	3.8	541	12	BH581366
9	38	3.8	1098	10	BF980551
10	38	3.8	1101	12	CNS0039G
11	37.8	3.8	725	12	AQ421725
12	37.8	3.8	945	9	AL544411
13	37.8	3.8	1281	12	AG075401
14	37.6	3.8	1477	12	AG043219
15	37.4	3.7	471	12	AZ113002
16	37.4	3.7	1101	12	CNS017V6
17	37.2	3.7	417	10	H46465

18	37.2	3.7	509	12	AQ123336	AQ123336 HS_3103-B
19	37.2	3.7	608	12	BH11363	BH11363 RPCI-24-4
20	37	3.7	238	9	BE183329	BE183329 RC4-HT066
21	37	3.7	253	12	BH292353	BH292353 CH230-186
22	37	3.7	350	12	CNS02E4E	AL193271 Tetradon
23	37	3.7	555	9	AV441208	AV441208 AV441208
24	37	3.7	769	12	CNS011WN	AL100817 Drosophila
25	37	3.7	775	12	BE909760	BE909760 601495915
26	37	3.7	1006	12	CNS00JMT	AL077129 Drosophila
27	36.8	3.7	273	9	BB514731	BB514731 BB514731
28	36.8	3.7	441	9	AI030202	AI030202 UT-R-CO-1
29	36.6	3.7	696	10	BI154298	BI154298 602905239
30	36.6	3.7	790	10	BF182476	BF182476 601804243
31	36.6	3.7	839	12	CNS004NB	AL054280 Drosophila
32	36.6	3.7	908	12	AZ549202	AZ549202 ENTGA10FE
33	36.6	3.7	1101	12	CNS00DY8	AL077393 Drosophila
34	36.6	3.7	1101	12	CNS0167A	AL077176 Drosophila
35	36.4	3.6	182	9	AI611686	AI611686 tui3h12.x
36	36.4	3.6	303	12	CNS00612	AL065493 Drosophila
37	36.4	3.6	519	10	C98216	C98216 C98216 Rice
38	36.4	3.6	737	10	BF294776	BF294776 008PBG01
39	36.4	3.6	861	9	AL548346	AL548346 AL548346
40	36.4	3.6	997	12	CNS006DN	AL065132 Drosophila
41	36.4	3.6	1010	12	CNS0167E	AL107180 Drosophila
42	36.4	3.6	1022	12	CNS003RM	AL064979 Drosophila
43	36.2	3.6	438	10	BM090853	BM090853 1916408.x
44	36.2	3.6	855	10	BI099897	BI099897 602885018
45	36.2	3.6	1594	10	BE962092	BE962092 601655164

ALIGNMENTS

RESULT 1
CNS00LT2/c
LOCUS
DEFINITION
CNS00LT2 1101 bp DNA linear GSS 14-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACRA8Bp19 of RPCI-98 library from Drosophila melanogaster (fruit fly) genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL078714.1 GI:5102004
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
JOURNAL
TITLE
COMMENT
Direct Submission
Submitted (11-JUN-1999) Genoscope - Centre National de Sequenc
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosier in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
Source
Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"

In the TJ loose lab at the University of California, Riverside total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A)⁺ RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million plv were in vivo excised to give pluescript SK⁻ cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Bequm, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of primed value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/Projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Clone TJ, Wing R, Kleinoffs A, Wise R (2001) genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.ipw.usda.gov/ggpages/bgng/31/clover.html>)"

```

BASE COUNT      270 a      424 c      220 g      184 t
ORIGIN
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site1: NotI; Site2: SalI; Cloned unidirectionally;
oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH-MGC Library."

```

Query Match	3.8%	Score 38	DB 10	Length 1098
Best Local Similarity	60.8%	Pred. NM. 96		
Matches	62	Conservative	0	Mismatches 40
				Indels 0
				Gaps 0
QY	888	gtcgcgtcacacgcttcgcgtgcgtgcacactctgctgtgcgcgcgaagaagga	947	
DB	902	GACTCCCCCCCCGACTCTCCCCCGCTCTCCCCACACACGTTGGCCCCCACACCAAGCGCGC	961	
QY	948	agaacgaacgcccgcacacacactaacacacgycacacactccc	989	
DB	962	ACACCCGCGCGCCACCCACCCACCGCCACGCGCACACCCCC	1003	

RESULT	10
CNS0039G	
LOCUS	1101 bp DNA linear GSS 03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence TE13 end of BAC # BARO8K10 of RPc1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL063921
VERSION	AL063921.1 GI:4941778
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 1101)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

COMMENT

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuhiro Oseegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and Est libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

```

FEATURES
source      location/Qualifiers
1. .1101   melanogaster"
/dbp.xref="taxon:7227"
/clone_11p="RRC1.98"
/clone="BACR08K10"
/note="end : TET3"
201 a      64 c    131 g    202 t    503 others
BASE COUNT
ORIGIN
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Query Match	3.8%	Score 38	DB 12	Length 1101
Best Local Similarity	14.0%	Pred. NO	96	
Matches 37	Conservative 132	Mismatches 95	Indels 0	Gaps 0

359 ctttccctctggaattcatagctcaactttttttaatggaagcaagtggtgcaa 418

[illegible]

RESULT	11
LOCUS	AQ421725
DEFINITION	AQ421725 725 bp DNA linear GSS 23-MAR-1998
ACCESSION	RPC1-11-190G1.TV RPC1-11 Homo sapiens genomic clone RPC1-11-190G1,
VERSION	DNA sequence.
KEYWORDS	AQ421725 AQ421725 . GI:4479449
SOURCE	GSS.
	human.

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 725)
REFERENCE AUTHORS	Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter , J.C.
TITLE	Use of BAC End sequences from Library RPI-11 for Sequence-Ready Map Building
JOURNAL	Unpublished (1997)
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@igf.org
Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@ejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.flygtr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES	
source	location/Qualifiers
1. .725	
/organism="Homo sapiens"	
/db_xref="GDB:7572720"	
/db_xref="taxon:9606"	
/clone="RPCT-11-190G1"	
/clone_11b="RPCT-11"	
/sex="Male"	
/cell_type="Lymphocytes"	
/note="Vector: pBACE3.6; Site_1: Rpool Human Male BAC Library"	
256 a	123 c 129 g 216 t
BASE COUNT	1 others
ORIGIN	

Query Match	3.8%;	Score 37.8;	DB 12,	Length 725;
Best Local Similarity	48.0%;	Pred. No. 1.1e+02;		
Matches 108; Conservative	0;	Mismatches 117;	Indels 0;	Gaps 0;

QY 449 ttctcaaacccatgacatgcaattctcaaacccatgacccgagagtcacatgcgagt 508

Accession	Sequence	Position
Db	TTAATAATTAAATTATACACTTTAAATATTAAAGATAATATCTACCAATTAAAGACATGA	465
Qy	gaacgaagaacttgaataatcaacatccagttgtccgagtcgagaagagatgacaatgaa	568
Db	TTATGGGATGGATTAATAAAACAAAGACCAAGTATATGTGTCTACAAAGAAACCCACTTAA	525
Qy	agtaacgattacagatttcattcatcacatgtaacaatatgataatgtaccataatt	628
Db	AATATAAAGACGTCTATTTCATATAATAGATGTGTGGAGAAAGACATGATATCTTAACACT	585
Qy	tgcttttcggaacagagtcggtgctcttttttttttcaacagaa	673
Db	AATCTAAAGGAAGCTTGTAGTAGCTTATATAATTATTAGACAGAA	630

FEATURES	source
AL544441.1	LOCUS
AL544441.1	DEFINITION
AL544441.1	ACCESSION
AL544441.1	VERSION
AL544441.1	KEYWORDS
EST.	SOURCE
human.	ORGANISM
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 945)	REFERENCE
L1,W.B., Gruber,C., Jessee,J. and Polayes,D.	AUTHORS
Full-length cDNA libraries and normalization	TITLE
Unpublished (2001)	JOURNAL
Contact: Genoscope	COMMENT
Genoscope - Centre National de Sequencage	
BP 191 91006 Evry cedex - France	
Email: seiret@genoscope.cns.fr, web : www.genoscope.cns.fr.	
Location/Qualifiers	
1..945	

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSOD1018Y18"
/clone_id="L1_NFL006.PL2"
/tissue_type="Placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8571
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

```

[illegible]

RESULT	13
LOCUS	AG075401
DEFINITION	Pan troglodytes DNA, clone: PTB-068E17.F., genomic survey sequence.
ACCESSION	AG075401
KEYWORDS	GSS; GSS (genome survey sequence).
SOURCE	Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Pan troglodytes BAC library clone:PTB-068E17.F. Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan. ORGANISM
REFERENCE	1 (sites)
AUTHORS	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., TotoKI,Y., Watanabe,H. and Sakaki,Y.
TITLE	BAC end sequences of library PTB
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1281) Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., TotoKI,Y., Watanabe,H. and Sakaki,Y.
AUTHORS	Direct Submission
TITLE	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenho-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimbesc@sc.riken.go.jp, URL:http://bgp.gsc.riken.go.jp/ Tel:-45-503-9111, Fax:-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
COMMENT	PRIMERS Sequencing: -21M13 LIBRARY Vector : pKS145 R.Site 1 : SacI R.Site 2 : SacI. Location/Qualifiers 1..1281 /organism="Pan troglodytes" /db_xref="taxon:9598" /clone="PTB-068E17.F." /sex="male" /cell_type="lymphoblast" /clone_lib="PTB Chimpanzee Male BAC Library"
FEATURES	source
BASE COUNT	285 a 491 c 460 g 26 t 19 others
ORIGIN	
Query Match	3.8%; Score 37.8; DB 12; Length 1281;
Best Local Similarity	56.6%; Pred. No.1,1e+02;
Matches	69; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
OY	868 ctctgctctccgcgaacgagcgttcgctctcacacgctcgctcgctgcacacctgctgct 927
Db	180 CCCCCCCCcCGCACCCGGCGGGCGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCAAG 239
OY	928 ggaggcgacgaagaagaaagaaagcaaacgcgcgcacacacactcacacggcacactcc 987
Db	240 GGCGGGAAGGCGGGGGGGCGCGCGCCGCCGCCGCCGCCGCCGGAACAACCGCGGCCG 299
OY	988 cc 989
Db	300 CC 301
RESULT	14
LOCUS	AG043219
DEFINITION	Pan troglodytes DNA, clone: PTB-021H12.F., genomic survey sequence.
ACCESSION	AG043219
KEYWORDS	GSS; GSS (genome survey sequence).
SOURCE	Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male

ORGANISM	BAC library clone: PTB-021H12.F.
REFERENCE	Eumariyola, Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan. 1 (sites)
TITLE	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Tokoki,Y., Watanabe,H. and Sakaki,Y.
JOURNAL	BAC end sequences of library PTB Unpublished 2 (bases 1 to 1477)
AUTHORS	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Tokoki,Y., Watanabe,H. and Sakaki,Y.
COMMENT	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpdes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel.:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors. PRIMERS Sequencing: -21M13
FEATURES	LIBRARY Vector : pKS145 R.Site 1 : SacI R.Site 2 : SacI. location/Qualifiers 1..1477 /organism="Pan troglodytes" /db_xref="taxon:9598" /clone="PTB-021H12.F." /sex="male" /cell_type="lymphoblast" /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT	446 a 382 c 525 g 83 t 41 others
ORIGIN	
Query Match	3.8%; Score 37.6; DB 12; Length 1477;
Best Local Similarity	55.1%; Pred.No.1.2e+02;
Matches 70; Conservative 0; Mismatches 57; Indels 0; Gaps 0;	
OY	808 gtactacgaggccgcgtcaaacggcatgcccgaagaagcgtccccaccgttttgcat 867
Db	937 gTGCCTGGGTGCCCGCCGCGGTGTCGGCGCGTGTGCTGCCGCTTTNTTNCGCCCG 878
OY	868 ctctgcttcctccgaacagcagcgctgcgtccacacctgcgttcgctgcacactcgtgt 927
Db	877 CGGCCCGCCCCCCTCTCGCGCGGCTTCTCCCTGTGCTGCTAFTNCTGGCGTTTC 818
OY	928 gccgcgcg 934
Db	817 GCGC GCG 811
RESULT 15	
LOCUS	AZ113002 471 bp DNA linear GSS 12-MAY-2000
DEFINITION	PtCI-23-13D17.TU PtCI-23 Mus musculus genomic clone PtCI-23-13D17,
ACCESSION	AZ113002
VERSION	AZ113002.1 GI:7772220
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eumariyola, Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 471)
AUTHORS	Zhao,S., Niemman,W., Feldblum,T., Malek,J., Shatsman,S., Akinet ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P., and Fraser,C.W.
TITLE	Mouse BAC End Sequences from Library PtCI-23

```

-JOURNAL
COMMENT
Unpublished (1999)
Other_GSSS: RPCI-23-13D17.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaoc@igf.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://BACPAC.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.figr.org/tdb/bac/ends/mouse/bac\_end\_intro.html
plate: 13 row: D column: 17
Seq primer: SP6
Class: BAC ends.
location/Qualifiers
1. .471
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-13D17"
/clone_1id="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site.1:
EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 132 a 129 c 97 g 113 t
ORIGIN
Query Match 3.7%; Score 37.4; DB 12; Length 471;
Best Local Similarity 62.1%; Pred. No. 1.3e+02;
Matches 59; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 375 attatagctcacactttttttaatggaacgaagtgccaaacacatcatttcaa 434
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 467 ATCTATCGGTACCGCATTTTATATGTAAACCAATAGTCTAGATCCCATGCGTTGTTG 408
QY 435 acaagaaataatcttccaacacacacatgacatg 469
| |||| |||| ||||| ||||| ||||| |||||
Db 407 AGGAGTAGGTAAAGAAATCAACCATCTCTGGGTTG 373

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 07:27:09 ; Search time 3917.59 Seconds
(without alignments)
5347.028 Million cell updates/sec

Title: US-09-508-377-10_COPY_4500_5500
1001
Sequence: 1 tactagcttaagattccca.....tgtattaacacagttgcgaca 1001

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_com:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sy:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	ID	Description
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1	1001	100.0	11463	6	AX031271	AX031271 Sequence
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5	131.6	13.1	102887	8	ATP17C15	AL162506 Arabidops
6	128.2	12.8	2853	8	TA066376	U66376 Trillium ae
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8	124.2	12.4	2726	8	AF338432	AF338432 Trillium
9	124.2	12.4	2970	8	AF286319	AF286319 Trillium
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ALIGNMENTS

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LOCUS AX031271 Sequence 10 from Patent WO9914314.
ACCESSION AX031271
VERSION AX031271.1 GI:10278603

KEYWORDS

SOURCE

ORGANISM

Aegilops tauschii.
Aegilops tauschii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Trilliceae; Aegilops.

REFERENCE

AUTHORS

TITLE

JOURNAL

1 (bases 1 to 11463)
Il, Z., Morell, M. and Rahman, S.
Regulation of gene expression in plants
Patent: WO 9914314-A 10 25-MAR-1999;
GOODMAN FIELDER LTD (AU) ; LI ZHONGYI (AU) ; MORELL MATTHEW (AU) ;
RAHMAN SADEOUR (AU) ; UNIV AUSTRALIAN (AU) ; COMM SCI ENT IND RES
ORG (AU) ; GROUPE LIMAGRAIN PACIFIC PTY L (AU)

FEATURES

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RESULT 2
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LOCUS 11475 bp DNA linear PLN 27-MAR-2001
DEFINITION Aegilops tauschii starch branching enzyme Iia gene, complete cds.
ACCESSION AF38431
VERSION AF38431.1 GI:13447949
KEYWORDS
SOURCE
ORGANISM Aegilops tauschii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Aegilops.
REFERENCE
1 (bases 1 to 11475)
Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,
Kosar-Hashemi, B., Abrahams, S. and Morell, M.K.
Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary
Relationships Among Isoforms. Characterization of a Gene for
Starch-Branching Enzyme Iia from the Wheat D Genome Donor Aegilops
tauschii
Plant Physiol. 125 (3), 1314-1324 (2001)
JOURNAL MEDLINE
PUBMED 21140316
REFERENCE 11244112
2 (bases 1 to 11475)
Rahman, S., Regina, A., Li, Z., Sharon, A. and Morell, M.K.
Direct Submission
Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,
Canberra, ACT 2601, Australia
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Db 4231	CAGGAAACCAAGATTAATATATATCCAACTTTAGAGATGATGTCTCCCGTATMAAA	4290		
QY 373	aggtctgatacaatgacagtgagataatgtaacccagagactctactatgacaagc	432		
Db 4291	AAGCTAGGCTATTAATGCTGTGACGATTAATGGCCATTTCAGAGCATGCTACTATGCCAC	4350		
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Db 4625	TGGCTTCTCTTAA 4638			

ACCESSION	AC006919	AF002093
VERSION	AC006919.5	GI:6598632
KEYWORDS	HTG.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 101365)	
AUTHORS	Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Beilto, M.-I., Town, C.D., Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldhahn, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Motaf, K.S., Cronin, L.A., Shen, M., VanAken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Tallon, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and Venter, J.C.	
TITLE	Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana	
JOURNAL	Nature 402 (6763), 761-768 (1999)	
MEDLINE	20083487	
PUBMED	10617197	
REFERENCE	2 (bases 1 to 101365)	
AUTHORS	Lin, X.	
TITLE	Direct Submission	
JOURNAL	Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA	
COMMENT	On Dec 17, 1999 this sequence version replaced gi:4581138.	

On Dec 17, 1999 this sequence version replaced gi:4581138. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site <http://www.tigr.org/cdb/at/at.html>.

Genes were identified by a combination of three methods: Gene prediction programs including GRAFT (<http://arthur.epm.ornl.gov/pub/graft/>), GeneFinder (Phil Green, University of Washington), GENSCAN (Chris Burge, <http://genome.stanford.edu/GENSCAN.html>), and NetPlantGene (<http://www.cbs.dtu.dk/services/NetGene2/>), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curation based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are annotated as tRNA-scan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNA-scan-SE/>). Simple repeats were identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/Mashu/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13J16, the ESSA group for sequencing clone F1304, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tsubata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especiallyixin Zhou, Hanif Khalek, Michael E. Henney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

Address all correspondence to: at@tigr.org.

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gene	HGFSEFAQDSIELVTLKMKPSTCLVSLDPEPTDVRRLTEYSELIDSGCPQNE	
gene	ASLSTIIPNSYFANLRMRKLESEFLKNPDDEGHOBQISHRTLPLSPSEYDIS	
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misc_feature	EMPEVEVELVELPLRNSIVGLPGVGLSTLQKRLTALVELVANGSIVIFMDEPTSG	
misc_feature	DLARRAAIVMTKRVYDTGTRVYCTIHPQSLIDFSEFLMLLMLKRGQVILVGLTGH	
misc_feature	HSQKIVVEFLIEGVPIKIDYNNPATMLDVTTPYSKMSQNSVFAQIFVNSVNRND	
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QY	673	ttgatcgtaagcagcagctgagctggtttgcttgccttattgattgattgctacatgtaa	732
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LOCUS	Arabidopsis thaliana	DNA chromosome 5,	BAC clone F17C15 (ESSA project).
DEFINITION	Arabidopsis thaliana	DNA chromosome 5,	BAC clone F17C15 (ESSA project).
ACCESSION	AL162506	GI:7340643	
KEYWORDS	thale cress.		
SOURCE	Arabidopsis thaliana		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE	1 (bases 1 to 102897)		
AUTHORS	Bevan, M., Pohl, T., Weizenegger, T., Bancroft, I., Mewes, H. W., Rudd, S., Lemcke, K. and Mayer, K. F. X.		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 102897)		
AUTHORS	EU Arabidopsis sequencing project.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 1a, D-82152 Martinsried, FRG, E-mail: lemcke@mpi-biochem.mpg.de, mayer@mpi-biochem.mpg.de, Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk		
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ .		
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sites AA541-551"
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exon
intron
exon

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Qy 366	aattaaaggcttggatcatatgcacgctgcagatataatgcaatccagagcatctacta 425
Db 30001	CATCAAAAAGCTGGATATATATGCTGTTCAATATATGCGCATACAGAACATTCATATTA 30060
Qy 426	tcgaagcttttggatattcaacaatccatttttctgtatataactctccaccattgg 485
Db 30061	TGCCAGCTTTGGGATATCTTTTAA-CCTTAGAGACTCTAGTAGAACCCTAGATATTTGC 30119
Qy 486	agctatcatatccatcatgcttcatatgcacataataaatttggatataaaccttattgat 545
Db 30120	ATTATATATATGTTGCACAACATAATGCGTTTATAGCGCTTTTATGACCATGATGCTATGTA 30179
Qy 546	atatagaacatacactatgattcttgaataaagatcatattat- 590
Db 30180	TCTTCACCAACTAGTATATAGATATGTCATATCTTATTTGTTTCTTACTAGAGAAC 30239
Qy 591	-----gtgttgctgtgtccaggtacacatgattactaatatttttgcaccaagtagcc 643
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Qy 644	gttttggacatccacaggaacttaaatctcttgcataagagacatagcttggttgc 703
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Db 30360	TAGTTCATGATGATTCCTTCATAGTAGTGA 30391
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LOCUS	TAU66376 2853 bp mRNA linear PLN 18-OCT-1996
DEFINITION	Triticum aestivum 1,4-alpha-D-glucan
ACCESSION	U66376
VERSION	U66376.1 GI:1620661
KEYWORDS	
SOURCE	wheat.
ORGANISM	Triticum aestivum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
AUTHORS	Kroeger,C., Loez,H. and Luetticke,S.
TITLE	1 (bases 1 to 2853)
JOURNAL	Direct Submission
	Submitted (08-AUG-1996) University of Hamburg, Institute of General Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr. 18, Hamburg 22609, Germany
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OY	373	aggcttgatcatcagcaggttcgaagtaatggaaccagagagcatcatcatcagcaagc	432						
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OY	433	tttggattccacaatcatcttttc	461						
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AF064560	2554	bp	mRNA	linear	PLN 03-NOV-1998				
LOCUS	AF064560	Hordeum vulgare cultivar Bomi starch branching enzyme I1a (sbe11a)							
DEFINITION	AF064560	mRNA, nuclear gene encoding plastid protein, complete cds.							
ACCESSION	AF064560.1	GI:3822019							
VERSION									
KEYWORDS									
SOURCE									
ORGANISM	barley.								
	Hordeum vulgare								
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
	Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;								
	Poideae; Triticeae; Hordeum.								
REFERENCE	1	(bases 1 to 2554)							
AUTHORS	Sun,C.,	Sathish,P.,	Ahlandsberg,S.	and	Jansson,C.				
TITLE	The two genes encoding starch-branching enzymes I1a and I1b are differentially expressed in barley								
JOURNAL	Plant Physiol. 118 (1), 37-49 (1998)								
MEDLINE	98404232								
REFERENCE	2	(bases 1 to 2554)							
AUTHORS	Sun,C.,	Sathish,P.,	Ahlandsberg,S.	and	Jansson,C.				
TITLE	Direct Submission								
JOURNAL	Submitted (11-MAY-1998) Stockholm University, Biochemistry,								
	Stockholm S-10691, Sweden								
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BASE COUNT 731 a 494 c 632 g 657 t
 ORIGIN

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QY	658	gaggaactaaatccctgcatcgtatagagacaatgagcttggttcgttgccttctatgat	717			
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QY	718	atgtgcatagtagtaattagtcacaaatttattttagctgttttaccgctt	766			
Db	940	attgttcattagtcattcctcctcaaatatattacccttgacggtttgaaatgagtt	988			

RESULT		8
LOCUS	AF338432	
DEFINITION	Triticum aestivum starch branching enzyme Iia variant mRNA,	2726 bp RNA linear PLN 27-MAR-2001
ACCESSION	AF338432	
VERSION	AF338432.1	
KEYWORDS	GI:13447951	
SOURCE	bread wheat.	
ORGANISM	Triticum aestivum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
AUTHORS	Poideaea; Triticeae; Triticum. 1 (bases 1 to 2726) Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M., Kosar-Hashemi,B., Abrahams,S. and Morell,M.K. Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary Relationships Among Isoforms. Characterization of a Gene for Starch-Branching Enzyme Iia from the Wheat D Genome Donor Aeigllops tauschii	
TITLE	Plant Physiol. 125 (3), 1314-1324 (2001)	
JOURNAL	Plant Physiol. 125 (3), 1314-1324 (2001)	
MEDLINE	21140316	
PUBMED	11244112	
REFERENCE	2 (bases 1 to 2726)	
AUTHORS	Rahman,S., Regina,A., Li,Z., Abrahams,S. and Morell,M.K.	
TITLE	Direct Submission	
JOURNAL	Submitted (18-JUN-2001) Plant Industry, CSIRO, Clunies Ross, Canberra, ACT 2601, Australia	
FEATURES	Location/Organisms 1..2726	
SOURCE	/organism="Triticum aestivum" /db_xref="taxon:4565" 124.. 2430 /note="SBELIA variant"	
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BASE COUNT
ORIGIN

726 a 564 c 701 g 735 t

[illegible]

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RESULT      9
LOCUS       AF286319                      2970 bp    mRNA    linear    PLN 30-OCT-2000
DEFINITION  Triticum aestivum starch branching enzyme 2 (Sbe2) mRNA, complete cds.
ACCESSION   AF286319
VERSION     AF286319.1
KEYWORDS    GI:11037533
SOURCE      bread wheat.
ORGANISM    Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideaee; Triticeae; Triticum.
REFERENCE   1 (bases 1 to 2970)
AUTHORS    McCue,K.F., Hurkman,M.J., Tanaka,C.K. and Anderson,O.D.
TITLE      Starch Branching Enzymes Sbe1 and Sbe2 from Wheat (Triticum
aestivum cv. Cheyenne): Molecular Characterization, Developmental
Expression, and Homolog Assignment by Differential PCR
Unpublished
2 (bases 1 to 2970)
AUTHORS    McCue,K.F. and Anderson,O.D.
TITLE      Direct Submission
JOURNAL     Submitted (11-JUL-2000) United States Department of Agriculture,
Agricultural Research Service, 800 Buchanan Street, Albany, CA
94710-1105, USA

FEATURES
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SOURCE	Oryza sativa.
ORGANISM	Oryza sativa. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriatloideae; Oryzeae; Oryza.
REFERENCE AUTHORS TITLE JOURNAL	1 (bases 1 to 3015) Baba,T., Kawasaki,T., and Ichikawa,N. NEW RICE GENE FOR STARCH-BRANCHING ENZYME Patent: JP 1998004970-A 1-13 -JAN-1998 MITSUI GROSAT SHOKUBUTSU BIO KENKYUSHO .KK, MITSUI PETROCHEM IND LTD
COMMENT	OS Oryza sativa (rice) PN JP 1998004970-A/1 PD 13-JAN-1998 PE 24-JUN-1996 JP 1996162983 PI BABA TADASHI , KAWASAKI TSUTOMU, ICHIKAWA NORIO PC C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/10,(C12N15/09, PC C12R1.91), PC (C12N5/10,C12R1.91),(C12N9/10,C12R1.19); CC strandedness: Double; topology: linear; FH Key Location/Qualifiers FT source 1..3015 FT organism='Oryza sativa' FT cultivar='Nihonbare' FT clone_lib='Rice Immature Seed Lambda gIII FT CDNA library' FT tissue_type='Immature seed' FT clone='PRB1' FT CDS 129..2654 FT product='branching enzyme-4' FT sig_peptide
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Matches 124;	Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Oy 313	caggaaeccgaaataattcatatgcttaatttagagtgaggtgtgccaaagaattaa 372
Db 1146	CCGGAAACCGAAGATTAAACAATATCTTAATTTTACGAGTAGAGTGCTCCACGAATTAAA 1205
Oy 373	aggacttgatataaatgcagtcagcagataatggcaaccggaacattcatatccaagc 432
Db 1206	AAGCTTGGGTCAATGCTGTACAGATAAATGGCAATTCACGAGACTCTTTATTACGCAAGC 1265
Oy 433	tttgggtattcacacaatccattttttic 461
Db 1266	TTTTGGGTATCATGTTACTAATCTTCTTGC 1294
RESULT 14	
LOCUS	ABO23498 3015 bp mRNA linear PIN 04-AUG-1999
DEFINITION	Oryza sativa mRNA for starch branching enzyme rbe4, complete cds.
VERSION	ABO23498.1 GI:5689137
KEYWORDS	starch branching enzyme rbe4, Oryza sativa tissue_lib:developing seeds cDNA to mRNA.
SOURCE	Oryza sativa Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehharitoidae; Oryzeae; Oryza.
ORGANISM	Mizuno,K., Tachibana,M., Kobayashi,E., Kawasaki,T., Funane,K., Kobayashi,M. and Baba,T. Molecular cloning and expression analysis of a novel member of
REFERENCE	
AUTHORS	
TITLE	

REFERENCE	JOURNAL	starch branching enzyme isoform in developing rice seeds
2 (bases 1 to 3015)	Unpublished (1999)	
Mizuno,K. and Baba,T.		
Direct Submission		
Submitted (09-FEB-1999)	Kouchi Mizuno, University of Tsukuba,	
Institute of Agricultural and Forest Engineering; 1-1-1 Tennoudai,		
Tsukuba, Ibaraki 305-8572, Japan		
E-mail:koumome@akura.cc.tsukuba.ac.jp, Tel:81-298-524656,		
Fax:81-298-55-2203		
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BASE COUNT	796 a 606 c 819 g 794 t	
ORIGIN		
Query Match	10.9% Score 109; DB 8; Length 3015;	
Best Local Similarity	83.2%; Pred. No. 1.6e-14;	
Matches 124; Conservative	0; Mismatches 25; Indels 0; Gaps 0;	
QY 313	cagggaaccgaagataaattacatgataatttagaggaatgaagtggtgccagaagataaa 372	
Db 1146	CCGGAACCGAAGATAAACACATATGCTAATTTTGAAGGATGAGGTGCTPACCAAGATTAA 1205	
QY 373	aggcttgatcatcaatgcagtcagatataatggcaatccaggagcattactactatgcaagc 432	
Db 1206	AAGCTTGGGTCAATGCTGTGACAGATATGGAATCCAGGAGCACTTTATTATGACCAAGC 1265	
QY 433	tttgagtataccacaatcatcttttc 461	
Db 1266	TTTGGGTATCATGTTACTAATCTCTTTC 1294	
RESULT 15		
ZM055948	ZM055948	
LOCUS	ZM055948 2795 bp mRNA linear PLN 21-AUG-1997	
DEFINITION	Zea mays starch branching enzyme I1a (sbe2a) mRNA, partial cds.	
ACCESSION	U65948	
VERSION	U65948.1 GI:2340107	
KEYWORDS		
SOURCE	Zea mays.	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE	1 (bases 1 to 2795)	
AUTHORS	Geo,M., Fisher,D.K., Kim,K.N., Shannon,J.C. and Guiltinan,M.J.	

TITLE Independent genetic control of maize starch-branching enzymes Ila and Iib. Isolation and characterization of a Spe2a cDNA
JOURNAL Plant Physiol. 114 (1), 69-78 (1997)
REFERENCE 97303618
AUTHORS 2 (bases 1 to 2795)
TITLE Gao, M., Fisher, D. K., Kim, K.-N., Shannon, J. C. and Gullinan, M. J.
JOURNAL Direct Submission
Submitted (02-AUG-1996) Hort./Biotech. Inst., Penn State University,
519 Wartik, University Park, PA 16802, USA

FEATURES
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1..2795
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ADLYLRGMQERDQAMQHLGKYEFTSDHSYVSRKHEDKVIIFERGLVVFNFHW
SNSIFDYRKGCFKPGKRYKIVLDSDDGLFEGFSRLDHDAREFTADWPHDNRPCSFVYA
PSRTAVVYAPAGAED"

gene
CDS

BASE COUNT 766 a 563 c 709 g 757 t
ORIGIN

Query Match 10.6%; Score 105.8; DB 8; Length 2795;
Best Local Similarity 81.9%; Pred. No. 8.2e-14;
Matches 122; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Db 929 CCGGAACCAAGATTAATGCTAACTTACGATGAGTGGCTTCCAGAAATTAA 988
QY 373 aggcctggatacatgcatgcaatgcaatccagagatcatcatatcatatgcaagc 432
Db 989 AACCTTGCATACATGACATGACATGACATGACATGACATGACATGACATGAC 1048
QY 433 ttgggtatcacacaatcatcttttc 461
Db 1049 TTTGGGTACCATGTTACGAATTTTTC 1077

Search completed: September 12, 2002, 07:29:49
Job time: 20777 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 08:21:02 : Search time 406.92 Seconds
(without alignments)
4223.512 Million cell updates/sec

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Sequence: 1 tactagcttaagattccca.....tgctataaccagttggaca 1001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1001	100.0	11473	20	AAK34650
2	965	96.4	11475	22	AAH78338
3	124.2	12.4	2726	22	AAH78337
4	112.2	11.2	8381	22	AAH78343
5	111.6	11.1	23449	21	AAZ35393
6	109	10.9	3015	19	AAV05638
7	107	10.7	2307	19	AAZ99938
8	105.4	10.5	2968	22	AAH78342
9	100.8	10.1	2087	18	AAH69737

C	10	100.8	10.1	2165	18	AAH69736	Corn starch branch
	11	100.8	10.1	2640	19	AAV70961	DNA encoding maize
	12	100.8	10.1	2665	18	AAH69729	Plasmid pBE240 ins
	13	100.8	10.1	2725	19	AAV29757	Zea mays starch br
	14	97.6	9.8	2919	19	AAQ73750	Rice starch branch
	15	95.4	9.5	1919	19	AAV38720	cDNA encoding star
	16	91	9.1	3090	19	AAV38720	Full length cassav
	17	88.6	8.9	2715	21	AAAC45939	Arabidopsis thalia
	18	88	8.8	2529	17	AAH42637	Class A starch bra
	19	88	8.8	2531	17	AAH17267	Class A starch bra
	20	88	8.8	2576	17	AAH42636	Class A starch bra
	21	88	8.8	2578	17	AAH42631	Class A starch bra
	22	88	8.8	3003	17	AAH42634	Class A starch bra
	23	88	8.8	3033	17	AAH42630	Class A starch bra
	24	88	8.8	3231	17	AAH42632	Class A starch bra
	25	87.6	8.8	3074	18	AAH69587	Potato starch bran
	26	84.8	8.5	2975	17	AAH42635	Class A starch bra
	27	83	8.3	2913	19	AAV38719	Full length cassav
	28	71.2	7.1	1809	18	AAH69753	Corn starch branch
	29	71.2	7.1	1865	18	AAH69748	Corn starch branch
	30	71.2	7.1	2487	18	AAH69747	Corn starch branch
	31	71.2	7.1	2565	18	AAH69752	Corn starch branch
	32	71.2	7.1	2713	19	AAV70962	DNA encoding maize
	33	71.2	7.1	2763	19	AAV29758	Zea mays starch br
	34	71.2	7.1	2771	13	AAQ24257	Branching enzyme D
	35	71.2	7.1	2772	18	AAH69740	Plasmid pBE65 inse
	36	71.2	7.1	8119	21	AAZ35392	Maize starch bran
	37	71	7.1	4563	22	AAH30910	Wheat starch bran
	38	68.8	6.9	604	21	AAH16018	Human prostate can
	39	68.8	6.9	2899	22	AAH02926	Human shear stress
	40	68.8	6.9	3075	24	AAH94880	Human DNA sequence
	41	66.6	6.7	2687	20	AAK34646	WBE I-D4 cDNA seq
	42	64.6	6.5	2733	15	AAQ54674	Rice starch branch
	43	64.6	6.5	12151	15	AAQ62135	Rice starch branch
	44	64.6	6.5	12151	15	AAQ62137	Rice starch branch
	45	63.4	6.3	11475	19	AAV54979	Potato starch bran

ALIGNMENTS

RESULT 1	AAK34650	AAK34650 standard; DNA; 11473 BP.
ID	AAK34650;	
XX		
AC	AAK34650;	
XX		
DT	05-JUL-1999 (first entry)	
XX		
DE	Starch branching enzyme II (SBE II) gene sequence.	
XX		
KW	Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBF; GBS;	
KW	starch branching enzyme; starch soluble synthase; debanching enzyme;	
KW	endosperm; wheat; barley; granule-bound synthase; gluconin; starch;	
KW	grain softness protein I; bacterial isomylase; glycogen synthase;	
KW	WBE I-D4 gene; ss.	
XX		
OS	Triticum tauschii.	
XX		
PN	WO9914314-A1.	
XX		
PD	25-MAR-1999.	
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PF	11-SEP-1998; 98WO-AU00743.	
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PR	20-MAR-1998; 98AU-0002509.	
PR	12-SEP-1997; 97AU-0009106.	
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PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
PA	(GOOD-) GOODMAN FIELDER LTD.	
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	
XX	(AUSU) UNIV AUSTRALIAN NAT.	

PI L1 2, Morell M, Rahman S;
 XX
 DR WPI; 1999-229525/19.
 XX
 PT New isolated cereal plant enzyme genes used for, e.g. expression of
 PT antisense sequences of granule bound synthase
 XX
 PS Claim 8; Page 75-81; 171pp; English.
 XX
 CC The invention relates to a novel enzyme of starch biosynthetic pathway
 CC in a cereal plant, where the enzyme is selected from starch branching
 CC enzyme (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching
 CC enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or
 CC SBE I of rice or maize. The methods and products can be used for
 CC targeting expression specifically to the endosperm of the seeds of cereal
 CC plants such as wheat or barley. They can be used for the expression of
 CC e.g. antisense sequences of granule-bound synthase (GBSS), SBE II, low
 CC mol. wt. glutenin, grain softness protein I, bacterial isomylase,
 CC bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They
 CC can be used for modifying the characteristics of starch produced by a
 CC plant. The present sequence represents the SBE II gene sequence.
 CC
 XX
 SQ Sequence 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 other;

Query Match 100.0%; Score 1001; DB 20; Length 11473;
 Best Local Similarity 100.0%; Pred. No. 3.6e-241;
 Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 agccattccctacttaataagagagagacaagagggggggggggggggggttccc 120
 DB 4570 agccattccctacttaataagagagagacaagagggggggggggggggggttccc 4629
 QY 121 ttcatattctgcgagcgatccaacaaacttcattgtctcgtaggtacgtactgcagg 180
 DB 4630 ttcatattctgcgagcgatccaacaaacttcattgtctcgtaggtacgtactgcagg 4689
 QY 181 atctcccatatgaagagagatagtaattcttgtaaccttggaacctgaagct 240
 DB 4690 atctcccatatgaagagagatagtaattcttgtaaccttggaacctgaagct 4749
 QY 241 tgaggcatcgataataatactatcatcacataacttagagagatgcattgaatttag 300
 DB 4750 tgaggcatcgataataatactatcatcacataacttagagagatgcattgaatttag 4809
 QY 301 tctgattctgcacaggaacgagaataatcatatgcttaattttaaggatgaggtgttg 360
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 QY 361 ccaagaatlaaaggcttgatgataatgacatgacgaataatggcattcagaagatcca 420
 DB 4870 ccaagaatlaaaggcttgatgataatgacatgacgaataatggcattcagaagatcca 4929
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 DB 4930 tactatgaagcttgggtatcacacaatcatctttctgtatacaactcttaacca 4989
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 DB 4990 ttggagctattacatccctaagtcttcagacataaataattggatataatcccttat 5049
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 DB 5050 tagatataataacacacacttagtattctgaaaaagatcatttatgtttgtgct 5109
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 DB 5110 ttgtccaggtacatgttactaatatttttgcacaaagtagccgtttggagctccaag 5169

QY 661 gactlaaatcttgatcatagatagagacatgagcttggttgcctgttcttaagataat 720
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 DB 5230 gttaatggttaatgaccttaatttttagcgttttaactgtttttctgtttcttaa 5289
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 DB 5350 caaatctagagctgacataaagaaatattggcaaaaactagagctgcaaaaataattt 5409
 QY 901 cccatcccaatgagcagggccctatcgcggaatatcttccatctatataatgtgcta 960
 DB 5410 cccatcccaatgagcagggccctatcgcggaatatcttccatctatataatgtgcta 5469
 QY 961 cgtactcttttctcaagatgataaaccagctgaca 1001
 DB 5470 cgtactcttttctcaagatgataaaccagctgaca 5510

RESULT 2
 AAH78338
 ID AAH78338 standard; cDNA; 11475 BP.
 XX
 AC AAH78338;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of a starch branching enzyme designated F2.
 XX
 KW Wheat; starch branching enzyme; BE1b; SBE; transgenic plant;
 KW starch biosynthetic pathway; amylopectin; F2; amylose; ss.
 OS Aegilops tauschii.
 OS
 PN WO200162934-A1.
 XX
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001WO-AU00175.
 XX
 PR 21-FEB-2000; 2000AU-0005742.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (GOOD-) GOODMAN FIELDER LTD.
 PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
 PI Morell M, Rahman S;
 DR WPI; 2001-570635/64.
 XX
 PT Nucleic acids encoding wheat starch branching enzyme IIB, useful for
 PT altering the amylose and amylopectin content of cereal plants, e.g.
 PT wheat and barley -
 XX
 PS Example 1; Fig 2; 103pp; English.
 CC The present sequence encodes a wheat starch branching enzyme of
 CC Aegilops tauschii, designated F2. A. tauschii is likely to be the
 CC ancestral D genome donor of wheat. Probes isolated from the present
 CC sequence were used to identify type II starch branching enzymes (SBEs)
 CC in wheat, especially BE1b. The BE1b nucleic acids may be used to
 CC genetically transform cereal plants such as wheat or barley and for
 CC altering their nutritional content by modulating the starch
 CC biosynthetic pathway to vary levels of amylopectin and/or amylose
 CC produced in the plant.
 XX
 SQ Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 11 other;

Query Match	96.4%;	Score 965;	DB 22;	Length 11475;
Best Local Similarity	99.4%;	Pred. NO. 3.8e-232;		
Matches 1000; Conservative	0;	Mismatches 1;	Indels 5;	Gaps 3;

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Db	4502	tactagcttaagattccccccttagagatgtaagaaatalgtacattggagcgtccacaga	4561
QY	61	agccattcttacctatttaattgagagagacaaggggggggggggggggttccc	120
Db	4562	agccattcttacctatttaattgagagagagacaaggggggggggggggggttccc	4621
QY	121	ttaattatctgcgagcgatccaanaacttcattgcttcgaggtcgtacgtcgaag	180
Db	4622	ttaattatctgcgagcgatccaanaacttcattgcttcgaggtcgtacgtcgaag	4681
QY	181	atcccccatatgaagagatagatgtaattttctgtaaccttggaaacctggaaacctgagct	240
Db	4682	atcccccatatgaagagatagatgtaattttctgtaaccttggaaaccttggaaacctgagct	4741
QY	241	tgaagcactgcgtataatactactccacaacttacttgaagatgcactgaa--attta	299
Db	4742	tgaagcactgcgtataataatactactccacaacttacttgaagatgcactgaaatttta	4801
QY	300	gtgtgatctctgcacaggaacccgaagataatcatactgctaaatttagggatgagtgct	359
Db	4802	gtgtgatctctgcacaggaacccgaagataatcatactgctaaatttagggatgagtggtt	4861
QY	360	gccaaagatttaaaagccttgtagatacaatgcaatgacgaataagacacccagagcattc	419
Db	4862	gccaaagatttaaaagccttgtagatacaatgcaatgacgaataagacacccagagcattc	4921
QY	420	atactatgcagaagcttgggtatcacacaacatccatttttctcgtataac--tcttcac	478
Db	4922	atactatgcagaagcttgggtatcacacaacatccatttttctcgtataacatcttcac	4981
QY	479	catttgaagctattacatccatagtcttaatgtagacataaataatttgatataatccctt	538
Db	4982	catttgaagctattacatccatagtcttaatgtagacataaataatttgatataatccctt	5041
QY	539	attgaataatagtagacaacacacacactagatctg---aaaagaatcttattgtgtg	595
Db	5042	attgaataatagtagacaacacacacactagatctgataatccgmaanaagaatcttattgtgtg	5101
QY	596	tgcgtgttccaggtaaccatglttaactatttcttgacacaaagtacccggtttgnaactc	655
Db	5102	tgcgtgttccaggtaaccatglttaactatttcttgacacaaagtacccggtttgnaactc	5161
QY	656	cagagagcttaaaatccctgtatcgataaggacaaagagcttggtttggtttcttaagg	715
Db	5162	cagagagcttaaaatccctgtatcgataaggacaaagagcttggtttggtttcttaagg	5221
QY	716	ataatgtctcataggaattatgttccaaatttaattttagctgcgttttaactgttatacgtgat	775
Db	5222	ataatgtctcataggaattatgttccaaatttaattttagctgcgttttaactgttatacgtgat	5281
QY	776	tctaaaggggaatttcaggccaattatgatacatctgttccaaagctaaagatgtagcgaagaatgta	835
Db	5282	tctaaaggggaatttcaggccaattatgatacatctgttccaaagctaaagatgtagcgaagaatgta	5341
QY	836	aattcaaaatctagaatgtgcatagaagaaatttggcaaaaacttagagatgtagcgaaaaataaa	895
Db	5342	aattcaaaatctagaatgtgcatagaagaaatttggcaaaaacttagagatgtagcgaaaaataaa	5401
QY	896	attttccatctcaaaatgtagcaggcccatgcgcgaataattttccattctataaatgtg	955
Db	5402	attttccatctcaaaatgtagcaggcccatgcgcgaataattttccattctataaatgtg	5461
QY	956	tgtcagctgtaactctttttctcagatgtatataaacacagtttgaaa	1001
Db	5462	tgtcagctgtaactctttttctcagatgtatataaacacagtttgaaa	5507

RESULT	3
AAH78337	
ID	AAH78337 standard; cDNA; 2726 BP

Query Match	Similarity	12.4%	Score	124.2	DB	22	Length	2726	
Best Local	Similarity	83.4%	Pred. No.	2,1e-21					
Matches	141	Conservative	0	Mismatches	26	Indels	0	Gaps	0
QY	596	gcttgcaggtacacatgtactaattttttgcacaaagtagccgctttggaactcca	657						
Db	1039	ggagagcttgggtacacatttactaattttttgcacaaagtagccgctttggaactcca	1098						
QY	658	gagagactaaatccctctgtacatagagacacagaaatgagcttggcttcttctatgat	717						
Db	1099	gagagactaaatccctctgtacatagagacacagaaatgagcttggcttcttctatgat	1158						
QY	718	attgtcatagtgtaatttagtccaatttaatttagctgttttactggttt	766						
Db	1159	attgtcatagtgtaatttagtccaatttaatttagctgttttactggttt	1207						
RESULT	4								
AAH78343									
ID	AAH78343	standard	DNA	8381	BP				
XX									
AC	AAH78343								
XX									

DT	26-NOV-2001 (first entry)
XX	
XX	Partial genomic sequence of wheat starch branching enzyme (BE1b) .
DE	
XX	
XX	Wheat: starch branching enzyme: BE1b; SBE; transgenic plant;
KW	starch biosynthetic pathway; amylopectin; amylose; ss.
XX	
OS	Triticum sp.
XX	
PN	WO200162934-A1.
XX	
PD	30-AUG-2001.
XX	
PF	21-FEB-2001; 2001WO-AU00175.
XX	
PR	21-FEB-2000; 2000AU-0005742.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	(GOOD-) GOODMAN FIELDER LTD.
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX	
PI	Morell M, Rahman S;
XX	
DR	WPI; 2001-570635/64.
XX	
PT	Nucleic acids encoding wheat starch branching enzyme I1b, useful for
PT	altering the amylose and amylopectin content of cereal plants, e.g.
PT	wheat and barley -
XX	
PS	Claim 6; Page 95-98; 103pp; English.
XX	
CC	The present sequence represents a partial genomic sequence of a wheat
CC	starch branching enzyme, designated BE1b. BE1b is a type II starch
CC	branching enzyme (SBE). The BE1b nucleic acids may be used to
CC	genetically transform cereal plants such as wheat or barley and for
CC	altering their nutritional content by modulating the starch
CC	biosynthetic pathway to vary levels of amylopectin and/or amylose
CC	produced in the plant.
XX	
QO	Sequence 8381 BP; 2134 A; 1788 C; 1829 G; 2608 T; 22 other;

RESULT	5
AAZ35393	
ID	AAZ35393 standard; DNA; 23449 BP.
XX	
XX	
AC	AAZ35393;
XX	
DT	27-MAR-2000 (first entry)
XX	
DE	Maize amylose-extender (Ae) gene encoding starch branching enzyme.
XX	

XX	OS	XX	Starch branching enzyme 11b; amylose-extender gene; Ae gene; maize; corn; promoter; expression control element; endosperm; transgenic plant; ss.
XX			Zea mays.
FH	Key	Location/Qualifiers	
FH	misc_signal	597..602	
FT		/tag= a	
FT		/note= "I box, conserved in RBCS genes"	
FT	repeat_unit	1475..1481	
FT		/tag= b	
FT		/note= "RY repeat, distal regulatory element"	
FT	misc_signal	1967..1973	
FT		/tag= c	
FT		/note= "Hex, conserved element found in plant histone gene promoters"	
FT	misc_signal	2593..2599	
FT		/tag= d	
FT		/note= "MRB box, motif essential for metal ion-dependent induction of metallothionein genes"	
FT	GC_signal	2666..2671	
FT		/tag= e	
FT	GC_signal	2738..2743	
FT		/tag= f	
FT	GC_signal	2831..2836	
FT		/tag= g	
FT	misc_signal	2838..2844	
FT		/tag= h	
FT		/note= "MRB box, motif essential for metal ion-dependent induction of metallothionein genes"	
FT	GC_signal	2874..2879	
FT		/tag= i	
FT	TATA_signal	2933..2936	
FT		/tag= j	
FT	CDS	3065..19659	
FT		/tag= k	
FT		/note= "contains introns"	
FT	exon	2965..3176	
FT		/tag= l	
FT		/number= 1	
FT	intron	3177..3282	
FT		/tag= m	
FT		/number= 1	
FT	exon	3283..3428	
FT		/tag= n	
FT		/number= 2	
FT	intron	3429..3672	
FT		/tag= o	
FT		/number= 2	
FT	exon	3673..3827	
FT		/tag= p	
FT		/number= 3	
FT	intron	3828..4913	
FT		/tag= q	
FT		/number= 3	
FT	exon	4914..5012	
FT		/tag= r	
FT		/number= 4	
FT	intron	5013..5088	
FT		/tag= s	
FT	exon	5089..5131	
FT		/tag= t	
FT		/number= 5	
FT	intron	5132..5327	
FT		/tag= u	
FT		/number= 5	
FT	exon	5328..5387	
FT		/tag= v	
FT		/number= 6	

FT	Intron	5388..5886	/tag= w	FT	/tag= au	FT	/tag= au
FT		/number= 6		FT	/number= 18	FT	/number= 18
FT	exon	5887..5967	/tag= x	FT	/tag= av	FT	18457..18534
FT		/number= 7		FT	/number= 19	FT	/tag= av
FT	Intron	5968..6048	/tag= y	FT	18535..18800	FT	/number= 19
FT		/number= 7		FT	/tag= av	FT	/tag= av
FT	exon	6049..6165	/tag= z	FT	/number= 19	FT	18801..18956
FT		/number= 8		FT	/tag= ax	FT	/tag= ax
FT	Intron	6166..6750	/tag= aa	FT	18957..19404	FT	/number= 20
FT		/number= 8		FT	/tag= ay	FT	/tag= ay
FT	exon	6751..6816	/tag= ab	FT	/number= 20	FT	/number= 20
FT		/number= 9		FT	19405..19479	FT	/tag= az
FT	Intron	6817..7591	/tag= ac	FT	/number= 21	FT	/number= 21
FT		/number= 9		FT	19480..19575	FT	19480..19575
FT	exon	7592..7713	/tag= ad	FT	/tag= ba	FT	/tag= ba
FT		/number= 10		FT	/number= 21	FT	/number= 21
FT	Intron	7714..8464	/tag= ae	FT	19576..19659	FT	19576..19659
FT		/number= 10		FT	/tag= bb	FT	/tag= bb
FT	exon	8465..8584	/tag= af	FT	/number= 22	FT	/number= 22
FT		/number= 11		FT	19843..19849	FT	19843..19849
FT	Intron	8585..12604	/tag= ag	FT	/tag= bc	FT	/tag= bc
FT		/number= 11		FT	23089..23101	FT	23089..23101
FT	exon	12605..12734	/tag= ah	FT	/tag= bd	FT	/tag= bd
FT		/number= 12		FT		FT	
FT	Intron	12735..12820	/tag= ai	FT		FT	
FT		/number= 12		FT		FT	
FT	exon	12821..12931	/tag= aj	FT		FT	
FT		/number= 13		FT		FT	
FT	Intron	12932..13079	/tag= ak	FT		FT	
FT		/number= 13		FT		FT	
FT	exon	13080..13208	/tag= al	FT		FT	
FT		/number= 14		FT		FT	
FT	Intron	13209..16259	/tag= am	FT		FT	
FT		/number= 14		FT		FT	
FT	exon	16260..16363	/tag= an	FT		FT	
FT		/number= 15		FT		FT	
FT	Intron	16364..17235	/tag= ao	FT		FT	
FT		/number= 15		FT		FT	
FT	exon	17236..17380	/tag= ap	FT		FT	
FT		/number= 16		FT		FT	
FT	Intron	17381..17837	/tag= aq	FT		FT	
FT		/number= 16		FT		FT	
FT	exon	17838..17985	/tag= ar	FT		FT	
FT		/number= 17		FT		FT	
FT	Intron	17986..18129	/tag= as	FT		FT	
FT		/number= 17		FT		FT	
FT	exon	18130..18230	/tag= at	FT		FT	
FT		/number= 18		FT		FT	
FT	Intron	18231..18458		FT		FT	

QY	309	tgcacggaacggaataatcatatgcttaatttagagatgagtggtgccaagaat	368	FT	/tag= au	FT	/tag= au
Db	7585	tgattggaacggaataacacatctgtaaacctttagtgatgagtcctccaagaat	7644	FT	18457..18534	FT	18457..18534
QY	369	taaaagcttgatataatgcagtgcaataatgccaatccagagacatcactatgc	428	FT	/tag= av	FT	/tag= av
Db	7645	aaaaaaacttgatacaatgcagtgcaataatgccaatccagagacatcactatg	7704	FT	/number= 19	FT	/number= 19
QY	429	aagcttgggtatcacacaatcatcttttctgcat	466	FT	18535..18800	FT	18535..18800
Db	7705	aagcttgggtatcacacaatcatcttttctgcat	7742	FT	/tag= av	FT	/tag= av

Query Match 11.1%; Score 111.6; DB 21; Length 23449;
Best Local Similarity 81.6%; Pred. No. 5.8e-18;
Matches 129; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

WPI; 2000-116538/10.
Gulltinan MJ, Kim K;
New gene regulatory sequences from plants used to provide resistance to
microbial path pathogens -

AAV05639
ID AAV05639 standard; cDNA to mRNA: 3015 BP.
AC AAV05639;
XX
DT 01-MAY-1998 (first entry)
XX
DE Rice type IV starch branching enzyme cDNA.

KX	Rice; type IV starch branching enzyme; amylopectin synthesis; ds.
KW	Oryza sativa.
OS	
XX	Key Location/Qualifiers
FH	CDS 129..2654
FT	/tag= a
FT	sig_peptide 129..287
FT	/tag= b
FT	mat_peptide 288..2651
FT	/tag= c
XX	/product= type_IV_starch_branching_enzyme
PN	JF10004970-A.
XX	
PD	13-JAN-1998.
XX	
XX	24-JUN-1996; 96JP-0162983..
XX	
PR	24-JUN-1996; 96JP-0162983.
XX	
PA	(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
RA	(MITK) MITSUI TOATSU CHEN INC.
DR	WP1; 1998-133625/13.
DR	P-PSDB; AAM41763.
XX	
PT	Rice starch branching enzyme gene - synthesises amylopectin to yield
XX	high quality starch
PS	Claim 4; Pages 5-8; 13pp; Japanese.
CC	The present sequence encodes the rice type IV starch branching
CC	enzyme, which has the ability to synthesise amylopectin. The
CC	quality of starch is improved by the use of the protein.
XX	
SQ	Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;
Query Match	10.9%; Score 109; DB 19; Length 3015;
Best Local Similarity	83.2%; Pred. NO. 1,4e-17;
Matches 124; Conservative	0; Mismatches 25; Indels 0; Gaps
QY	313 caggaaaccgaagataaaatcatalgtctaattttagagatgagtgttgccaagaataaa 372 Db 1146 ccgaacgcgaagataaacacatatgtcaatttttaggatgaggttgtactcaagaattaa 1205
OY	373 aggttgatatacatgagcgagcataatgycataccagaagcatctacatcaagc 432 Db 1206 aagctctggatcaaatgtctgacgaataatlygcataccagaacacatctattaacgaagc 1265
OY	433 tttagtatcacacaatccatttttc 461 Db 1266 tttagtatcatgttacttaactctttgc 1294
RESULT 7	
AAZ99938	standard; DNA; 2307 BP.
AC	
XX	AAZ99938;
DT	25-JUL-2000 (first entry)
XX	
DE	DNA encoding part of starch branching enzyme II clone 5A1.
XX	
KW	Wheat; starch branching enzyme II; SBEII; SBEII-1; starch;
KW	gelatinisation onset; transgenic plant; foodstuff; bakery product; ss
XX	Triticum aestivum.
SH	Key Location/Qualifiers

FT	CDS.	1..2307
FT	/tag=	a "starch branching enzyme II"
FT	/product=	"starch branching enzyme II"
FT	/transl_except-	(pos: 2036..2038, aa: Xaa)
FT	/transl_except-	(pos: 2051..2053, aa: Xaa)
FT	/transl_except-	(pos: 2051..2053, aa: Xaa)
FT	/transl_except-	(pos: 2090..2092, aa: Xaa)
FT	/transl_except-	(pos: 2096..2098, aa: Xaa)
FT	/transl_except-	(pos: 2114..2116, aa: Xaa)
FT	/transl_except-	(pos: 2147..2149, aa: Xaa)
FT	/transl_except-	(pos: 2168..2170, aa: Xaa)
FT	/transl_except-	(pos: 2174..2176, aa: Xaa)
FT	/transl_except-	(pos: 2189..2191, aa: Xaa)
FT	/transl_except-	(pos: 2267..2269, aa: Xaa)
FT	/transl_except-	(pos: 2270..2272, aa: Xaa)
FT	/transl_except-	(pos: 2306..2307, aa: Asn)
FT	/note=	"Xaa is an unknown amino acid; the sequence contains 10 internal stop codons, but no termination codon"
FT		
PD	WO200015810-A1.	
PD	23-MAR-2000.	
XX		
XX	09-SEP-1999;	99WO-GB03011.
XX		
PR	10-SEP-1998;	98EP-0307337.
XX		
PA	(PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.	
XX		
PI	Goldsbrough A, Collier S;	
DR	WPI, 2000-271446/23.	
XX	P-PSDB; AAYB4408.	
PT	DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature -	
PT		
XX		
XX	Disclosure: Fig 10; 197pp; English.	
CC	The present sequence encodes a wheat starch branching enzyme II (SBEII) of a novel subclass of known SBEII genes, designated SBEII-1. The SBEII-1 genes are thought to have similar functional properties to the maize SBEII gene. Starch branching enzymes catalyse the formation of the alpha-1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the preparation or processing a foodstuff, particularly bakery products.	
SO	Sequence 2307 BP: 674 A; 440 C; 544 G; 635 T; 14 other:	
Query Match	10.7%; Score 107; DB 21; Length 2307;	
Best Local Similarity	71.0%; Pred. No. 4, 2e-17;	
Matches 157; Conservative 0; Mismatches 60; Indels 4; Gaps 1		
OY	220 cctacttggaacctgagcgttgaggcatcgcttaatatatcatcatcataacttagt 279 	
Db	228 ccgaagagggagaagtatgatccaacaccctcaacctaaagacca-----aatcatgc 283 	
OY	280 aggaatgacatcgaattttgltgltgltgltgltgacagagccgaagataatcatatgt 339 	
Db	284 cgatatatagaacaacatgttggcatgtagcccggaaccaagtaacaacatatgca 343 	
OY	340 aattttaggagtgaggtgtgtgccaaagaattaaggccttgatatacatgcatgcatgata 399 	
Db	344 aacttcagaggaatgaggtgtgtccaaagaattaaggccttgatatacatgcatgcatgata 403 	
OY	400 atgcgaatccagagcatcatcatcatctgcaacttggata 440	

Db 404 atggcaatccagagcaccatcactatgtgaagcttggta 444

RESULT 8

AAH78342
ID AAH78342 standard; cDNA; 2968 BP.

AC AAH78342;

DT 26-NOV-2001 (first entry)

DE Nucleotide sequence of wheat starch branching enzyme (BE1B).

KW Wheat; starch branching enzyme; BE1B; SBE; transgenic plant;

KW starch biosynthetic pathway; amylopectin; amylose; ss.

OS Triticum sp.

PN WO200162934-A1.

PD 30-AUG-2001.

PF 21-FEB-2001; 2001WO-AU00175.

PR 21-FEB-2000; 2000AU-0005742.

PA (CSTR) COMMONWEALTH SCI & IND RES ORG.

PA (GOOD-) GOODMAN FIELDER LTD.

PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

PI Morell M, Rahman S;

DR WPI; 2001-570635/64.

XX Nucleic acids encoding wheat starch branching enzyme IIB, useful for

PT altering the amylose and amylopectin content of cereal plants, e.g.

PT wheat and barley -

XX Claim 6; Fig 9; 103pp; English.

XX The present sequence encodes a wheat starch branching enzyme,

CC designated BE1B. BE1B is a type II starch branching enzyme (SBE).

CC The BE1B nucleic acids may be used to genetically transform cereal

CC plants such as wheat or barley and for altering their nutritional

CC content by modulating the starch biosynthetic pathway to vary levels

CC of amylopectin and/or amylose produced in the plant.

XX Sequence 2968 BP; 784 A; 626 C; 796 G; 756 T; 6 other;

SO Query Match 10.5%; Score 105.4; DB 22; Length 2968;

Best Local Similarity 70.6%; Pred. No. 1.1e-16;

Matches 156; Conservative 0; Mismatches 61; Indels 4; Gaps 1;

Db 220 cccacttggaacttgagcttgagcgcgtcaatatatactatcaactaacttag 279

Db 1101 ccgaagaaggaggtatgtatcaacatcctcaacaaagcaca--aaatcatgt 1156

QY 280 aggatcatggaatttagtgccttgacacaggaaccgaagataaatttatgtc 339

Db 1157 cggatataaacaacatgttgcagtgcagccggaacaaagatcaacacatatgca 1216

QY 340 aattttaggagtgagtggtgccaagaatbaaaggcttgatcacatgagtcagata 399

Db 1217 aattcagggatgagtggtcctcaagaatbaaaggcttgatcacatgagtcagata 1276

QY 400 atgccaatccaggaagcatcattatgcaagcttgggta 440

Db 1277 atgccaatccaggaagcatcattatgcaagcttgggta 1317

RESULT 9

AAH69737
ID AAT69737 standard; DNA; 2087 BP.

AC AAT69737;

DT 10-SEP-1997 (first entry)

DE Corn starch branching enzyme IIB gene fragment in pBE96.

KW Starch branching enzyme IIB; SBE1B; corn; maize; antisense;

KW amylopectin; transgenic plant; pBE96; ss.

OS Zea mays.

PN WO9722703-A2.

PD 26-JUN-1997.

PF 12-DEC-1996; 96WO-US19678.

PR 20-DEC-1995; 95US-0009113.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Broglie KE, Hubbard NL, Klein TM;

DR WPI; 1997-341694/31.

XX Transgenic corn in which grain derived starch fine structure is

PT controlled - specifically branch chain distribution of amylopectin,

PT useful in preparation of thickened foodstuff

XX Example 4; Page 56-57; 92pp; English.

XX A cDNA insert (AAH69737) in plasmid pBE96 comprises a 2.09 kb

CC fragment of corn starch branching enzyme IIB (SBE1B) cDNA (see

CC also AAH69729), starting at the initiating ATG codon of the coding

CC region and terminating 312 bp 5' of the translation termination

CC codon. It was obtd. by site-specific mutagenesis of the SBE1B

CC gene in plasmid pBE240 to generate an NcoI site at the ATG start

CC site, and EcoRI digestion of the mutagenised plasmid. The 2.09 kb

CC fragment was inserted, in sense orientation, between the zein

CC promoter and 3' regions in vector pMI103 to produce pBE96.

CC Co-suppression and antisense techniques can be used to inhibit

CC SBE1B in transgenic plants and thereby alter starch properties.

XX Sequence 2087 BP; 565 A; 396 C; 553 G; 573 T; 0 other;

SO Query Match 10.1%; Score 100.8; DB 18; Length 2087;

Best Local Similarity 57.4%; Pred. No. 1.5e-15;

Matches 201; Conservative 0; Mismatches 147; Indels 2; Gaps 1;

QY 127 atcttcgagcgatcacaacttcacatgtcttcgagtggtactgaaggatctcc 186

Db 707 atcttcacatcaggaagaagatcattccagcctcgatcaagatctcagtcagccc 766

QY 187 cattataagaagatat--agttaattcttgaaccttctggaacttgagcttgag 244

Db 767 caggagaataaccatatgtgaggtattatgatcctcctggaaggtaaagtatgt 826

QY 245 gcatcgctaataatactatcatcacaaataactaaggagatgcctcgaatttagtg 304

Db 827 tcagagatgcgcaaccctaaacgcaaaatcattgcgatatatgaacacatgcgaa 886

QY 305 atcttcacagagaacggaataatcattatgcttaatttagtgagtggtgcca 364

Db 887 tgagtgcgcggaacccgaataataacacatatgttaactttagtggtgaagtcctccaa 946

QY 365 gaattaaaggcttgatcaatgcagtcagatgaatgaatggcaatccaggaatcattact 424

Db 947 gaataaaaacttgatcaatgcagtcagatgaatgaatggcaatccaggaatcattact 1006

SQ Sequence 2725 BP; 727 A; 534 C; 715 G; 749 T; 0 other;

Oy	127	atctcgagcgatccaacaaatccatctggtctgagtgtaagctactgcaggatctcc	186
Db	797	atactccatcaggataaagatccaatccatccagcctgatacaagtactcagtcaggccc	856
Oy	137	catatgaagagabatatgtaattcttctgttaacctactgtgaaacttgagcttgag	244

Db	857	caggagaataacatcatgatgaggatttatatgatccctctgaagaggttaagatgtgt	916
Qy	245	gcacgcgttaatatatactatcatcacaaactactagaagatgtgcatctgaaatttagtgt	304
Db	917	tcaaggacagcgcaacctaaacgccaataatcatctggagataatyaacaacatgtcggaa	976
Qy	305	atcttcgcacagaaacggaagataatcatatgtctaatcttggagatgaagtgtrtccaa	364
Db	977	tgaatgaccgcgaaccgaagataacaacatagttaaaccttggagatgaagtcctcccaa	1036
Qy	365	gaattaaaaagccttggatataatgcagtgctgaagtaatgtcaatccaagaagcatcatact	424
Db	1037	gaataaaaaaaccttggatataatgctgcagtcgaaataatgtcaatccaagaagcatcatact	1096
Qy	425	atgcaagccttggatattcacacaatccattttttctgtatacaactct	474
Db	1097	atgaaagccttggatattcacagtaactaatcttcttgcgcaagtgtcgt	1146

ID AAQ73750 standard; cDNA to mRNA; 2919 BP.

DT 05-JUL-1995 (first entry)

DE Rice starch branching enzyme.

KW Starch branching enzyme; rice; starch content; ds.

Oryza sativa.

FH	Key	Location/Qualifiers
----	-----	---------------------

ET

ET

ET

FT 3'UTR

XX

XX

XX

XX

PR	29-OCT-1992;	92JP-0291719.
XX		
PA	(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.	
XX		
DR	WPI; 1994-337418/42.	
XX		
DR	P-PSDB; AAR60811.	
XX		
PT	New gene of branching enzyme of rice starch - useful for	
PT	Increasing starch yield of rice grains	
XX		
PS	Claim 1; Page 9-12; 13pp; Japanese.	
XX		
CC	The rice starch branching enzyme is encoded by the cDNA sequence	
CC	AAQ373750. The starch content of rice grains can be increased by	
CC	increasing the expression of branching enzyme in rice plants.	
XX		
SQ	Sequence 2919 BP; 755 A; 590 C; 800 G; 774 T; 0 other;	
Query Match	9.8%; Score 97.6; DB 15; Length 2919;	
Best Local Similarity	75.6%; Pred. No. 1e-14;	
Matches 121; Conservative	0; Mismatches 39; Indels 0; Gaps 0;	
QY	315 ggaaccgaagataaattcatatgacctaatttagggatgaggtgtccaaagaattaaaag 374	
DB	1102 ggagcccaagatcaacacacgtatgcaacctttagggatgaggtgtccaaagaattaaa 1161	
QY	375 gcttgatatacatgtcagtgacagataatggtcaatccaggagcatcattacatgcaagctt 434	
DB	1162 gcttgatatacatgtcagtgacagataatggtcaatccaggagcatcattacatgcaagctt 1221	
QY	435 tgggtattcacacaatccattttttctgtataaccttt 474	
DB	1222 tgggtattcacacacaaatttcttctgcaacaaagtatcgt 1261	
RESULT 15		
ID	AAV38722 standard; DNA; 1919 BP.	
XX		
AC	AAV38722;	
XX		
DT	21-SEP-1998 (first entry)	
DE	cDNA encoding starch branching enzyme II (SBE II).	
XX		
KW	Starch branching enzyme; SBE; cassava; ss.	
XX		
OS	Manihot esculenta.	
XX		
FH	Key Location/Qualifiers	
FT	CDS 61..1506	
FT	/*tag= a	
FT	/product= SBE II	
FT	1507..1900	
FT	/*tag= b	
XX		
XX	WO9820145-A2.	
PN		
PD	14-MAY-1998.	
XX		
PF	04-NOV-1997; 97WO-GB03032.	
XX		
PR	05-NOV-1996; 96GB-0023095.	
XX		
PA	(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.	
XX		
PI	Jobling SA, Safford R;	
XX		
DR	WPI; 1998-286958/25.	
DR	P-PSDB; AAM62650.	
XX		
XX	Starch branching gene from cassava - useful for producing altered	

PT plants giving modified starch
 XX
 PS Claim 9; Fig 10; 67pp; English.
 XX
 CC The present sequence encodes starch branching enzyme (SBE) II. It
 CC was isolated from cassava tubers. The products can be used for
 CC producing plants having altered starch quantities and qualities.
 CC They can also be used for producing altered plants such as cassava,
 CC banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
 CC and rice plants.
 XX
 SQ Sequence 1919 BP; 543 A; 324 C; 467 G; 585 T; 0 other;

Query Match 9.58; Score 95.4; DB 19; Length 1919;
 Best Local Similarity 78.6%; Pred. No. 3.2e-14;
 Matches 114; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 584 ttattgttgctgctgtccaggtacatgttactaatttttgcaccaagtggc 643
 |||||
 Db 44 tttttttttttgttgtagtttgggtacacatgtcacaaacttttgcacttagcagcc 103
 QY 644 gtttggaaactccagaggaactaaacacctgatacgaatagacacatgagcttggttc 703
 |||||
 Db 104 gatttgaactccctgatgatgttggaagctttaataagataaagctcatgagtttaggctgc 163
 QY 704 ttgtcttatagtatgttcatag 728
 |||||
 Db 164 ttgtctcatgtatgttcatag 188

Search completed: September 12, 2002, 08:21:51
 Job time: 12268 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 08:12:27 ; Search time 92.79 Seconds
(Without alignments)
2649.845 Million cell updates/sec

Title: US-09-508-377-10_COPY_4500_5500
1001

Perfect score: 1 tactagcttaagattccca.....tgtatracacagttggaca 1001

Sequence: 1 tactagcttaagattccca.....tgtatracacagttggaca 1001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCrUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.8	10.1	2725	US-08-941-445A-14	Sequence 14, Appl
2	87.6	8.8	3074	US-09-087-277-1	Sequence 1, Appl
3	86	8.6	1393	US-09-087-277-3	Sequence 3, Appl
4	71.2	7.1	2763	US-08-941-445A-16	Sequence 16, Appl
5	63.4	6.3	11478	US-08-981-803-29	Sequence 29, Appl
6	63.4	6.3	11478	US-08-983-440-29	Sequence 29, Appl
7	61.8	6.2	2909	US-08-104-158-1	Sequence 1, Appl
8	61.8	6.2	3128	US-08-716-449-1	Sequence 1, Appl
9	54	5.4	807	US-08-165-315D-1	Sequence 1, Appl
10	54	5.4	807	US-08-702-609A-2	Sequence 2, Appl
11	54	5.4	846	US-08-165-315D-2	Sequence 2, Appl
12	54	5.4	1327	US-08-165-315D-3	Sequence 3, Appl
13	39.2	3.9	4467	US-08-565-907A-1	Sequence 1, Appl
14	39.2	3.9	4467	US-08-910-551B-1	Sequence 1, Appl
15	39.2	3.9	4467	US-08-909-425A-1	Sequence 1, Appl
16	38.6	3.9	8700	US-08-392-625-16	Sequence 16, Appl
17	38.6	3.9	8700	US-08-466-961A-16	Sequence 16, Appl
18	38.6	3.9	8700	US-08-645-193B-18	Sequence 18, Appl
19	37.4	3.7	7218	US-08-232-463-14	Sequence 14, Appl
20	37	3.7	84495	US-09-797-906-3	Sequence 3, Appl
21	35.8	3.6	1131	US-08-951-924A-1	Sequence 1, Appl
22	35.8	3.6	1131	US-09-172-339-3	Sequence 3, Appl
23	35.8	3.6	1131	US-09-420-211-10	Sequence 10, Appl
24	35.8	3.6	2426	US-08-528-026C-3	Sequence 3, Appl
25	34.8	3.5	870	PCT-US95-13658-3	Sequence 3, Appl
26	34.2	3.4	1921	US-08-557-128-11	Sequence 11, Appl
27	34.2	3.4	8133	US-08-480-604A-5	Sequence 5, Appl

28	34.2	3.4	8133	US-08-405-496A-5	Sequence 5, Appl
29	34.2	3.4	8133	US-08-935-136-5	Sequence 5, Appl
30	34	3.4	834	US-08-998-416-534	Sequence 534, App
31	33.8	3.4	398	US-08-714-918-5	Sequence 5, Appl
32	33.8	3.4	398	US-09-265-315-5	Sequence 5, Appl
33	33.8	3.4	398	US-09-265-315-5	Sequence 5, Appl
34	33.8	3.4	398	US-09-265-315-5	Sequence 5, Appl
35	33.8	3.4	4093	US-07-861-458C-5	Sequence 5, Appl
36	33.6	3.4	1185	US-08-179-557-14	Sequence 14, Appl
37	33.6	3.4	1680	US-09-242-690A-14	Sequence 14, Appl
38	33.4	3.3	312	US-09-242-690A-8	Sequence 8, Appl
39	33.4	3.3	662	US-08-998-416-185	Sequence 185, App
40	33.4	3.3	663	US-08-998-416-191	Sequence 191, App
41	33.4	3.3	665	US-08-998-416-937	Sequence 937, App
42	33.4	3.3	701	US-08-998-416-701	Sequence 701, App
43	33.4	3.3	711	US-08-998-416-786	Sequence 786, App
44	33.4	3.3	724	US-08-998-416-683	Sequence 683, App
45	33.4	3.3	732	US-08-998-416-1036	Sequence 1036, App

ALIGNMENTS

```
RESULT 1
US-08-941-445A-14
: Sequence 14, Application US/08941445A
: Patent No. 6107060
: GENERAL INFORMATION:
: APPLICANT: Keeling, Peter
: APPLICANT: Guan, Hanping
: TITLE OF INVENTION: Starch Encapsulation
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
: STREET: 5370 Manhattan Circle
: CITY: Boulder
: STATE: CO
: COUNTRY: US
: ZIP: 80303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/941,445A
: FILING DATE: 30-SEP-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/026,855
: FILING DATE: 30-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Winner, Ellen P
: REGISTRATION NUMBER: 28,547
: REFERENCE/DOCKET NUMBER: 89-97
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 499-8080
: TELEFAX: (303) 499-8089
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2725 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: not relevant
: MOLECULE TYPE: mRNA
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: Zea mays
: FEATURE: sig_peptide
: NAME/KEY: 91..264
: FEATURE:
: NAME/KEY: mat_peptide
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LOCATION: 265..2487
FEATURE:
NAME/KEY: CDS
LOCATION: 91..2490
US-08-941-445A-14

Query Match 10.1%; Score 100.8; DB 3; Length 2725;
Best Local Similarity 57.4%; Pred. No. 5.9e-19;
Matches 201; Conservative 0; Mismatches 147; Indels 2; Gaps 1;

QY 127 attctgcagcgtatcaaaactccattgtctcgaagtgtaactgcaggatctcc 186
DB 797 ATACTCCATCAGGAGATTAAGAGATTCAATTCCAGCCTGGATCACTACAGTCAGAGGCC 856
QY 187 catatgaagagagat--agttatctctgttaacctgtgaactgtgaactgtgag 244
DB 857 CAGAGAGAAATTCATATGATGGGATTATATGATCTCTCGAAGAGGTAAGATATGTGT 916
QY 245 gcacgcctaataatactatcatcacatactagagatgacatcgtgaatttagtg 304
DB 917 TCAGGCATGCGCAACCTAAACGACCAAAATGATGCGGATATATGAAACACATGTCGGA 976
QY 305 atcttcacagcagcagcgaagataatcatatgcttaattttagagtgaggtgtgccaa 364
DB 977 TGACTACCCGCAACCAAGATTAACACATATGTAACCTTAGGAGATGAACTCTCCCAA 1036
QY 365 gaataaagcgttgatataatgcagtcgagataatgcagcagcagagatctact 424
DB 1037 GAATTAATAAACTTGATATACATCACTGCAATATGCAATCCAGAGACTCATATTT 1096
QY 425 atgcaagcttgggtatcacacatccatttttctgtatacactct 474
DB 1097 ATGGAAGCTTGGATACCATGTACTATTTTTCGCGCAAGATGCGT 1146

RESULT 2
US-09-087-277-1
; Sequence 1, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087, 277B
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beli gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; FEATURE:

NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1

Query Match 8.8%; Score 87.6; DB 4; Length 3074;
Best Local Similarity 73.0%; Pred. No. 3.1e-15;
Matches 111; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 598 gctgttcacagtaaccatgtactaattttttgacacagtagccgtttggaactcca 657
DB 1374 gtagtttggtatcatcgtcacaaatttttngcaccaagcgcgttttgaancc 1433
QY 658 gaggaactaaatcccttgatcgatagagacatgagcttgctgttctatgag 717
DB 1434 gacgaccttagcttggatgataaagctcatgagctggaattgttctcatgac 1493
QY 718 atgttcataggaattagccaatttaatt 749
DB 1494 atgttccagcagcatgcatcaataataacttt 1525

RESULT 3
US-09-087-277-3
; Sequence 3, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087, 277B
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393


```

TYPE: DNA
ORGANISM: Unknown
FEATURE:
  OTHER INFORMATION: Description of Unknown Organism:deiI gene fragment
  OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
  OTHER INFORMATION: (potato)
FEATURE:
  NAME/KEY: CDS
  LOCATION: (2)..(1393)
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: (442)..(424)
  OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
  OTHER INFORMATION: C, G or T.
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: (422)..(424)
  OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: (890)..(892)
  OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
  OTHER INFORMATION: or Phe.
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: (1148)..(1150)
  OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-087-277-3

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	Query Match	8.6%	Score 86	DB 4	Length 1393
	Best Local Similarity	72.4%	Prod. No. 6.4e-15		
	Matches 110	Conservative	0	Mismatches 42	Indels 0
				Gaps	0
OY	538	gctgttcacaggtacacatgttactaatctttttgcacacagtcacgcttttgaactca	657		
Db	368	gctaattttgtgtacacatgcacaaatttttngccacacagcgcgttttgaanccc	427		
OY	658	gagagccttaaaatccttgcatacgatgacacatgagctgttgcgtttccttaagat	717		
Db	428	gacgacaccttaagctcttgcattgataaagctacatgagctagatgtgttcctcatgac	487		
OY	718	attgttcataagtgtaattggtccaatttaatt	749		
Db	488	attgttcacacgcacatgcacataataattctt	519		

US-RSULT 4
US-08-941-445A-16
Sequence 16 Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanning
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentm Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941.445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:

```

1 APPLICATION NUMBER: US 60/026,855
2 FILING DATE: 30-SEP-1996
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Winner, Ellen P
5 REGISTRATION NUMBER: 28,547
6 REFERENCE/DOCKET NUMBER: 89-97
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: (303) 499-8080
9 TELEFAX: (303) 499-8089
10 INFORMATION FOR SEQ. ID NO.: 16:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 2763 base pairs
13 TYPE: nucleic acid
14 STRANDEDNESS: single
15 TOPOLOGY: not relevant
16 MOLECULE TYPE: mRNA
17 HYPOTHETICAL: NO
18 ORIGINAL SOURCE:
19 ORGANISM: Zea mays
20 FEATURE:
21 NAME/KEY: transit_peptide
22 LOCATION: 2..190
23 FEATURE:
24 NAME/KEY: mat_peptide
25 LOCATION: 191..2467
26 FEATURE:
27 NAME/KEY: CDS
28 LOCATION: 2..2470
29 US-08-941-445A-16

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[illegible]

```

      RESULT 5
US-08-981-803-29
; Sequence 29, Application US/08981803
; Patent No. 6147279
; GENERAL INFORMATION:
; APPLICANT: POULSEN, PETER
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2004
; CURRENT APPLICATION NUMBER: US/08/981, 803
; CURRENT FILING DATE: 1997-04-17
; EARLIER APPLICATION NUMBER: PCT/EP96/03052
; EARLIER FILING DATE: 1996-07-12
; EARLIER APPLICATION NUMBER: 9514435. 8
; EARLIER FILING DATE: 1995-07-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2. 0
; SEQ ID NO 29
; LENGTH: 11478
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-981-803-29

Query Match      6.3%; Score 63.4; DB 3; Length 11478
Best Local Similarity 70.2%; Pred. No. 3.3e+08;

```


Db 233 TGACATAAACAATAATTACCCATCATAAATGACACAAAATATTTCACC 184

RESULT 12

US-08-165-315D-3/c
Sequence 3, Application US/08165315D
Patent No. 5525716

GENERAL INFORMATION:

APPLICANT: Odd-Arne Olsen
APPLICANT: Roger Kalla
TITLE OF INVENTION: Promoter
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: St. Onge, Steward, Johnston & Reens
STREET: 986 Bedford Street
CITY: Stamford
STATE: Connecticut
COUNTRY: U.S.A.
ZIP: 06905

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,315D
FILING DATE: 10 December 1993
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324707.0
FILING DATE: 2 December 1993

ATTORNEY/AGENT INFORMATION:

NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 2105-P0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-324-6155
TELEFAX: 201-327-1096
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 1327
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
DESCRIPTION: gene
FRAGMENT TYPE: gene
FEATURE:
NAME/KEY: Ltp2 gene
US-08-165-315D-3

Query Match 5.4%; Score 54; DB 1; Length 1327;
Best Local Similarity 68.2%; Pred. No. 6e-06;

Matches 75; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 793 gcaattatgtaacttgcataaagctgaagtcgcaagaatgcataaactctgaag 852

Db 293 GGAATGGAATTAATTATTTTCAACCTAAGAGTGGCAAAACTGCAAACTGCAAACTAGAG 234

Qy 853 tggcataagaagaattggcaaaactgaagtcgcaaaactaaatatttc 902

Db 233 TGACATAAACAATAATTACCCATCATAAATGACACAAAATATTTCACC 184

RESULT 13

US-08-565-907A-1/c
Sequence 1, Application US/08565907A
Patent No. 5814499

GENERAL INFORMATION:

APPLICANT: Sylvain Molineau, Barbara
APPLICANT: J. Holler, Peter A. Vandenberg,
APPLICANT: Ebenezer R. Vedamuthu, Jeffrey K.

APPLICANT: Kondo

TITLE OF INVENTION: DNA Encoding Phage

TITLE OF INVENTION: Abortive Infection Protein

TITLE OF INVENTION: From Lactococcus

TITLE OF INVENTION: Lactis, and Method of use thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZIP: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 kb storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS (version 4)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/565,907A
FILING DATE: December 1, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 3814499e

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 4467
TYPE: Nucleotide
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis

STRAIN:
INDIVIDUAL ISOLATE: W1
DEVELOPMENTAL STAGE: N/A
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: Bacterium
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE:

LIBRARY: genomic

CLONE: SMO-20

POSITION IN GENOME: N/A

FEATURE:

NAME/KEY: phage abortive infection

LOCATION: N/A

IDENTIFICATION METHOD: sequencing

OTHER INFORMATION: DNA encoding phage

OTHER INFORMATION: resistance

PUBLICATION INFORMATION: N/A

US-08-565-907A-1

Query Match 3.9%; Score 39.2; DB 1; Length 4467;

Best Local Similarity 44.9%; Pred. No. 0.14; Indels 0; Gaps 0;

Matches 149; Conservative 0; Mismatches 183; Indels 0; Gaps 0;


```

1 ADDRESSSEE: Ian C. McLeod
2 STREET: 2190 Commons Parkway
3 CITY: Okemos
4 STATE: Michigan
5 COUNTRY: USA
6 ZIP: 48864
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Diskette 5.25 inch,
9 MEDIUM TYPE: 360 kb storage
10 COMPUTER: Acer
11 OPERATING SYSTEM: MS-DOS (version 4)
12 SOFTWARE: wordperfect 5.1
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/909,425A
15 FILING DATE: August 11, 1997
16 CLASSIFICATION: 435
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 08/565,907
19 FILING DATE: December 1, 1995
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Ian C. McLeod
22 REGISTRATION NUMBER: 20,931
23 REFERENCE/DOCKET NUMBER:
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (517) 347-4100
26 TELEFAX: (517) 347-4103
27 TELEX: No. 5928688e
28 INFORMATION FOR SEQ ID NO: 1:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 4467
31 TYPE: Nucleotide
32 STRANDEDNESS: Single
33 TOPOLOGY: Linear
34 MOLECULE TYPE:
35 DESCRIPTION: Genomic DNA
36 HYPOTHEetical: NO
37 ANTI-SENSE: NO
38 FRAGMENT TYPE: N/A
39 ORIGINAL SOURCE:
40 ORGANISM: Lactococcus lactis
41 STRAIN:
42 INDIVIDUAL ISOLATE: W1
43 DEVELOPMENTAL STAGE: N/A
44 HAPLOTYPE: N/A
45 TISSUE TYPE: N/A
46 CELL TYPE: bacterium
47 CELL LINE: N/A
48 ORGANELLE: N/A
49 IMMEDIATE SOURCE:
50 LIBRARY: genomic
51 CLONE: SMO-20
52 POSITION IN GENOME: N/A
53 FEATURE:
54 NAME/KEY: phage abortive infection
55 LOCATION: N/A
56 IDENTIFICATION METHOD: sequencing
57 OTHER INFORMATION: DNA encoding phage
58 OTHER INFORMATION: resistance
59 PUBLICATION INFORMATION: N/A
60
61 US-08-909-425A-1

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Query Match	3.9%	Score 39.2;	DB 2;	Length 4467;
Best Local Similarity	44.9%;	Pred. No. 0.14;		
Matches 149;	Conservative 0;	Mismatches 183;	Indels 0;	Gaps 0;
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Db	2359	TATTTCTCATATTTTTAGACTACTCTTTTTTTTTTGTTTCATGTATTGTTATAACGGGA	2300	
Oy	517	aaatatgtgatataatccattatagtagtatagaacaactgaactgttaactcgaaa	576	
Db	2299	AAATCAATTTTATACCTCCTATTATCCCAAAATGTTCTTCATTGCACACATATATCATATA	2240	

Oy	577	aagtcatttatatggttggtgtttccaaagtaccagttacctaatttttgcaca	636
Dd	2239	AATGCTTATTCTTTTAATCCACTGTGCTGGAAATTAGTTGAATAATATTTTAAAAA	21800
Oy	637	agtagcogtttggaaactccagaagactaaatcccttcatcgatagacacatgaact	696
Dd	2179	AAGAAAAAATACCGATTTCGATTTTATCACAACAGCGGAAATTTGCACATTTTCGTT	21200
Oy	697	ggttgtcttgccttaatgatbatgttcatbaaggtaattagtcocaatlaattagctgt	756
Dd	2119	TATTATCATTTAATTAATTAAGCTTATTTTTCGCAGCAATTGATTAATTCATTTAAAAAAT	20600
Oy	757	tttacgtttatctcgtatcttcaagaagaaat	788
Dd	2059	CTTGCTTTTCATTTCTCAAAGAATTAACGGAAT	2028

Search completed: September 12, 2002, 08:12:56
Job time: 14833 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 08:10:10 : Search time 3207.55 Seconds

(without alignments)
4212.078 Million cell updates/sec

Title: US-09-508-377-10_COPY_4500_5500

Perfect score: 1001

Sequence: 1 tactagcttaagattccca.....tgtattaaccagcttgaca 1001

Scoring table: IDENTITY_NUC

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

EST:*
1: em_estha:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125.8	12.6	678	9	AV939010
2	104.8	10.5	375	10	BG240463
3	100.8	10.1	639	9	AM065909
4	92.2	9.2	386	12	CNS00SBA
5	89	8.9	491	12	BH521642
6	73.4	7.3	320	10	L37476
7	68.8	6.9	749	10	BE905170
8	68.2	6.8	595	12	BH022954
9	66.6	6.7	593	10	BG132327
10	65.2	6.5	868	10	BF272517
11	63.8	6.4	679	9	AU061011
12	63	6.3	375	10	C68665
13	63	6.3	573	10	BJ109423
14	63	6.3	637	10	BJ116696
15	62.4	6.2	487	10	BF704392
16	62.4	6.2	529	9	AA896824
17	62.4	6.2	716	9	BE055519

18	62.4	6.2	914	10	BG917939
19	62.4	6.2	2738	11	AK009815
20	61.8	6.2	751	10	BI920158
21	60.8	6.1	685	10	BE614098
22	60.6	6.1	243	10	C94562
23	60.2	6.0	466	10	BG350414
24	59.8	6.0	863	9	AT552716
25	58.8	5.9	566	10	BI642658
26	58.4	5.8	706	9	AT386274
27	57.2	5.7	887	12	AZ686939
28	57.2	5.7	896	12	BH150681
29	57.2	5.7	927	12	BH134897
30	56.6	5.7	555	9	AT452088
31	55.8	5.6	460	9	AA919922
32	55.8	5.6	648	10	BG762693
33	55.8	5.6	711	10	BI693151
34	55.8	5.6	786	9	AU002729
35	55.6	5.6	852	12	AZ530400
36	55	5.5	495	9	AT614714
37	54.8	5.5	613	9	AA444799
38	54.4	5.4	616	9	AU006028
39	53.6	5.4	360	10	D36576
40	53.6	5.4	1043	12	CNS0145P
41	53.4	5.3	447	12	AZ924939
42	52.8	5.3	985	12	CNS07801
43	52.6	5.3	531	9	AA786861
44	52.2	5.2	387	10	Z14737
45	52.2	5.2	928	12	CNS00DKY

ALIGNMENTS

RESULT 1
AV939010
LOCUS
DEFINITION AV939010 K. Sato unpublished cDNA library, strain H602 adult,
heading stage top three leaves Hordeum vulgare subsp. spontaneum
CDNA clone bah20e24 5', mRNA sequence.
AV939010
AV939010.1 GI:18234807

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 678)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
SOURCE
Location/Qualifiers
1..678
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="bah20e24"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/issue_type="top three leaves"
/dev_stage="adult, heading stage"
135 a 154 g 194 t 2 others

BASE COUNT
ORIGIN
193 a 135 c 154 g 194 t 2 others

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Oy	305	atcttcgacaggagaccgaagaataatcatatgcatactttagggatgaggttggtccaa	364
Db	417	TGAGTAGGCCGCGGAACCGAAGAATAAACACATATGTATAACTTATAGGATGAAGCTCCCAA	476
Oy	365	gaattaagaagcttgcgtatcaccaatgtcagcgccgatattatgccaatccagagactttatct	424
Db	477	GAAATAAAAAACCTTGATATACATATGACATGCAAAATATATGGCAATCCAAAGCAGCTCATATT	536
Oy	425	atgcgaagcttgcgggttatccacaacatccatctttcttcgtataacctttc 474	
Db	537	ATTGCAAGCTTTTGATATACATGTAATCTATTTTTTTGGCCCAAGTAGTGTCT 586	
RESULT	4		
CNS00SBA			
LOCUS		CNS00SBA	386 bp DNA linear GSS 28-JUN-1999
DEFINITION		Arabidopsis thaliana genome survey sequence T7 end of BAC TH18 of TAMU library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	
ACCESSION		AL088180	
VERSION		ALI088180.1	GI:5289320
KEYWORDS		GSS.	
SOURCE		Thale cress.	
ORGANISM		Arabidopsis thaliana	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.	
AUTHORS		Salanoubat,M., Cholsne,N., Artiguenave,F., Brotlter,P., Wincker,P., Samson,D., Saurin,W., Weissenbach,J. and Quetier.F.	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 386)	
AUTHORS		Genoscope.	
TITLE		Direct Submision	
JOURNAL		Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)	
FEATURES		- Web : www.genoscope.cns.fr	
SOURCE		location/Qualifiers	
		1..386	
		/organism="Arabidopsis thaliana"	
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		/db_xref="taxon:3702"	
		/clone_lib="RAMU"	
		/clone="TJH18"	
		/note="end : 77"	
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Best Local Similarity		57.5%; Pred. NO.3.6e-09;	
Matches 218; Conservative		0; Mismatches 138; Indels 23; Gaps 2;	
Oy	379	ggaatcaatgcagtgcagataaaygccaatccagsgaacattcatctatgcagacttg 438	
Db	1	GGATTAATGCGTGTCAATATATGSCCATFACAGAACATTCATATTATGCCCAGCTTGGG 60	
Oy	439	tattcacacaatcatttttttcgtataacactttcccccattgygagctatcatacc 498	
Db	61	TATTCCTTTTAA-CCTTAAGTAGACCTAGTAGAACCCCTGATATTTTGCAATTAATTGCT 119	
Oy	499	taatgcttcacagcaataaataatttgtatataaacccttattagatatatagtaacct 558	
Db	120	TGCACAACTATACGCTTTTAGGCTTTGTACCATGATGCTAGCTGTATCTCAAGCAACT 179	
Oy	559	aacacttagtatctgaaaaagatactattatgt-----ttgtt 596	
Db	180	AGTACTATATGATATCTCAATTCATTATGTGGTTTCTTACTGAGGAACAATGGCCATTTCIA 239	
Oy	597	ggcctgttcacgataccatgltacctaatttttttgacacaagtagccgttttgaaactc 656	

D	b	240	TTATGAAATGCAGGACGTACCAACTTTTTCGCCCAAGCAGTGCGCTGGGACC	299
Oy		657	agaagacttaaatcccttgatcgatagagacacatgaagtctggtttgccttcta	716
D	b	300	AGAGAACAATAAATCACATGATAGATAGAGAGCTACAGAGATTAGCCGTGTA	359
Oy		717	tattgttcataagcacaatta	735
D	b	360	TATCGTTCATAGTAGTA	378
RESULT		5		
LOCUS		BH521642	491 bp DNA	linear GSS 13-DEC-2001
DEFINITION		BOGTD277R BOGT Brassica oleracea genomic clone BOGTD27, DNA		
ACCESSION		BH521642		
VERSION		BH521642.1 GI:17729727		
KEYWORDS		GSS.		
SOURCE		Brassica oleracea.		
ORGANISM		Brassica oleracea		
REFERENCE		Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta: eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.		
AUTHORS		1 (bases 1 to 491)		
TITLE		Tom,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.		
JOURNAL		Whole genome shotgun sequencing of Brassica oleracea unpublished (2001)		
COMMENT		Other.GSSs: BOGTD27TF Contact: Chris Town		
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		/organism="Brassica oleracea"		
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		/clone="BOGTD27"		
		/clone_lib="BOGT"		
		/note="Vector: pHD31. Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHD31 using BstXI linkers"		
BASE COUNT		144 a 89 c 99 g 159 t		
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		Best Local Similarity 80.6%; Pred. No. 1,6e+08;		
		Matches 104; Conservative 0; Mismatches 25; Indels 0; Gaps 0;		
Oy		312 acagaaccagagaaattcatatgctcaatttagaggatagtggtgccaagaattaa	371	
D	b	294 ACAGGAACCAATGATTAATACATATGCCAACCTTTRAGAGATATGTACTCCCCGATATAA	353	
Oy		372 aaagcttgatatacaatgcagctgcagataatgccaatgccaggaatcatactatgcag	431	
D	b	354 AAAGCTAGAGATATATGCTGTTACAGATATATGCGCATTCACAGACATCTCTACTATGACAG	413	
Oy		432 cttagtgata 440		
D	b	414 CTTTGGGTA 422		
RESULT		6		
LOCUS		LJ37476	320 bp mRNA	linear EST 23-OCT-1996
DEFINITION		BNESTFCQ Mustard flower buds Brassica rapa cDNA clone F0956, mRNA		
		sequence.		

ACCESSION L37476
VERSION L37476.1 GI:887054
KEYWORDS EST.
SOURCE Brassica rapa.
ORGANISM Brassica rapa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 320)
AUTHORS Lim,C.O., Kim,H.Y., Kim,M.G., Lee,S.I., Chung,W.S., Park,S.H.,
Hwang,I. and Cho,M.J.
TITLE Expressed sequence tags of Chinese cabbage flower bud cDNA
JOURNAL Plant Physiol. 111 (2), 577-588 (1996)
MEDLINE 96255495
COMMENT Contact: Lim,C.O., Kim,M.G., Hwang,I. and Cho,M.J.
Plant Molecular Biology and Biotechnology Research Center
Email: pmbrchongae.gnu.ac.kr.
FEATURES
source Location/Qualifiers
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/strain="pekinensis"
/db_xref="taxon:3711"
/clone="F0956"
/clone_lib="Mustard flower buds"
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Best Local Similarity 72.5%; Pred. No. 2.8e-05;
Matches 95; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
OY 598 gctttccaggtaccatcttaatttttttcaccacaagaccggtttggaactcca 657
||| | | ||| ||| ||| ||| ||| | | ||| ||| ||| ||| ||| ||| ||| |||
DB 6 GCTAGCTTGGGTATCATATTAACAACCTTTCCCTCCCTAGCAGCCGCTTTGAGACACCT 65
OY 658 gaggaactaaatccttgatcgatagagacatgagcttgcttgcttctatgat 717
||| | | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 66 AATGACCTTAACCTTTATATAGCAAGCCTAGAGCTGCTGCTGCTCTTAATGAT 125
OY 718 attgttcataag 728
|||| | | |
DB 126 AATTGTGCACAG 136
RESULT 7
BE905170 749 bp mRNA linear EST 20-OCT-2000
LOCUS BE905170
DEFINITION 601499362P1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901214 5',
mRNA sequence.
ACCESSION BE905170
VERSION BE905170.1 GI:10398185
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 749)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM9701 row: 1 column: 15
High quality sequence stop: 691.

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/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 225 a 137 c 165 g 222 t
ORIGIN
Query Match 6.9%; Score 68.8; DB 10; Length 749;
Best Local Similarity 63.1%; Pred. No. 0.00024;
Matches 106; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
OY 309 tgcacaggaaccgaagataatcatatgctaattttagggatggtgtgccagaat 368
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DB 327 TTCCCATGAGAGAAAGTAGCTTCTTATTAACATTTTACATGCATGTACTCCAGAAAT 386
OY 369 taaaggcttgatatacatatgcagtcagataatggcaatccagagcatctataatgc 428
||| | | ||| ||| ||| | | | | | | | | | | | | | | | | | | | | | |
DB 387 CAAGGCTTGGATGATCAACTGCATTCAGTTCAGTATGCAGCAATCATGACATGCTTACTATGC 446
OY 429 aagcttggtatctacacatccatlttttctgtataactctca 476
||| ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 447 CAGCTTTGGTTACCAAAATCAAGGCTTCTTGACCTTCACGCGTTA 494
RESULT 8
BH022954/C 595 bp DNA linear GSS 29-JUN-2001
LOCUS BH022954
DEFINITION GH_MBB0003022r Gossypium hirsutum L. Gossypium hirsutum genomic
clone GH_MBB0003022r, DNA sequence.
ACCESSION BH022954
VERSION BH022954.1 GI:14577242
KEYWORDS GSS.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 595)
AUTHORS Tomkins,J.P., Peterson,D.G., Yang,T.J., Main,D., Wilkins,T.A.,
Paterson,A.H. and Wing,R.A.
TITLE Development of Genomic Resources for Cotton (Gossypium hirsutum
L.): BAC Library Construction, Preliminary SRC Analysis, and
Identification of Clones Associated With Fiber Development
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 569.
FEATURES
source Location/Qualifiers
1..595
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/cultivar="Maxxa"
/db_xref="taxon:3635"
/clone="GH_MBB0003022r"
/clone_lib="Gossypium hirsutum L."
/tissue_type="Young leaves"
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/note="Vector: pCGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation, ordering clones

SOURCE		Dicystostelium discoidum.
ORGANISM		Dicystostelium discoidum
REFERENCE		Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium. 1 (bases 1 to 679)
AUTHORS		Morito,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,, Yoshino,R., Mitera,B.N., Pl.M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y. Developmental cDNA in Dictyostelium discoidum unpublished (1998)
TITLE JOURNAL COMMENT		Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 3-3-10 Ten-noda, Tsukuba, Ibaraki 305, Japan Email: d40zhuesakura.cc.tsukuba.ac.jp PROJECT = Dictyostelium discoidum cdna project In Japan.
FEATURES		location/qualifiers
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	/strain="AX4"	
	/db_xref="taxon:44689"	
	/clone="SLC606"	
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	/dex_stage="slug"	
BASE COUNT	202 a 107 c 162 g 208 t	
ORIGIN		
Query Match	6.4%:	Score 63.8; DB 9; Length 679;
Best Local Similarity	67.9%:	Pred. No. 0.0026;
Matches	89; Conservative	0; Mismatches 42; Indels 0; Gaps 0;
OY	gctgtgccagtgaccatgtaactaattttggcaccaagtgcgttgtgaacctcoa	657
Db	GCATCGTTGTGGTATCAAGTCACGAATTCTTGTCGATCACGACGAGAATTGGCACACCG	307
OY	gaggaaacataaaccttatcgatagaacaacatatgctgtgttcctcgtlctttaigat	717
Db	GAGGAGTTGTAAGACATAATGATTAACCCACACGAGATGGCATTTGTGGTTTTTAGAC	367
OY	attgtccatag 728	
Db		
Db	GTGTGCCATVAG 378	
RESULT 12		
C68665 LOCUS	C68665	375 bp mRNA linear EST 23-SEP-1997
DEFINITION	C68665 yuji kohara unpublished cDNA Caenorhabditis elegans CDNA clone YK306c3 5', mRNA sequence.	
ACCESION VERSION KEYWORDS	C68665 C68665.1 GI:2430021	
ORGANISM SOURCE	EST. Caenorhabditis elegans. Caenorhabditis elegans Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea; Peloderinae; Caenorhabditis.	
REFERENCE AUTHORS	1 (bases 1 to 375) kohara,y., Motobashii,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano ,M., Miyata,A. and Nishigaki,A. Expression map of the C.elegans genome Unpublished (1996) Contact: Yuji Kohara Genome Biology Lab. National Institute of Genetics Yata 1111, Mishima, Shizuoka 411, Japan Tel.: 81-559-81-6854 Fax: 81-559-81-6855 Email: yokohara@lab.nig.ac.jp. Location/Qualifiers	
JOURNAL TITLE COMMENT		1..375
FEATURES		/organism="Caenorhabditis elegans" /strain="CB1469 him-8(eI489)" /db_xref="taxon:6239"
SOURCE		

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		Best Local Similarity		63.6%	Pred. No. 0.0039;				
		Matches 96;		Conservative 0;	Mismatches 55;	Indels 0;	Gaps 0;		
BASE COUNT	103 a	72 c	90 g	110 t					
ORIGIN									
Oy	322	aagataaatcatatgacgaattttagggatagaggtgtgccaaagaatataaagcttga	381						
Db	76	AAATTTACACATATCGGAATTCGCTCTACACATGTCTTCCGAGATACAAAGCAAGCA	135						
Oy	382	tacatgcagtcgataatgagcaatccagagacatcatctatgaagcttgggtat	441						
Db	136	TACAAATGCAATTCACGTTATGCGACGTGATGAGCAGCTTTATTATGATCATTTGGATAT	195						
Oy	442	tcacacaatccattttctctgtaacac	472						
Db	196	CAGGTTTGAACTTTTCGCTGTTTCCAGTC	226						
RESULT 13									
BI109423									
LOCUS	BI109423	573 bp	mRNA	Linear	EST 23-JAN-2002				
DEFINITION	BI109423 unpublished oligo-capped cDNA library, C. elegans L1 stage								
ACCESSION	Caenorhabditis elegans cDNA clone YK1119C01 5', mRNA sequence.								
VERSION	BI109423								
KEYWORDS	BI109423.1 GI:18269452								
SOURCE	EST.								
ORGANISM	Caenorhabditis elegans.								
	Caenorhabditis elegans.								
	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea								
	; Rhabditidae; Pelodierinae; Caenorhabditis.								
REFERENCE	1 (bases 1 to 573)								
AUTHORS	Kohara,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.								
	and Sugano,S.								
TITLE	A complementary view of the C.elegans genome								
JOURNAL	Unpublished (2002)								
COMMENT	Contact: Tadasu Shin-1								
	Center for Genetic Resource Information								
	National Institute of Genetics								
	1111 Yata, Mishima, Shizuoka 411-8540, Japan								
	Tel: 81-559-81-6856								
	Fax: 81-559-81-6855								
	Email: tshini@genes.nig.ac.jp.								
FEATURES	Location/Qualifiers								
Source	1..573								
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	/strain="N2"								
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	elegans L1 stage"								
	/sex="hermaphrodite"								
	/tissue_type="whole animal"								
	/dev_stage="L1"								
BASE COUNT	169 a	121 c	127 g	155 t	1 others				
ORIGIN									
Query Match									
6.3%, Score 63; DB 10; Length 573;									
Best Local Similarity 63.6%; Pred. No. 0.0039;									
Matches 96; Conservative 0; Mismatches 55; Indels 0; Gaps 0;									
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Db	309	AAATTTACACATATCGGAATTCGCTCTACACATGTCTTCCGAGATACAAAGCAAGCA	368						

Oy	382	tacaatgcagtcataatgcaatccgaacgtcattactatgcaagcttggatat	441
Dd	369	TACATTCGCAATTTCAGTTATGGCAGTGTATGCAGCACCGTTTATTATTCATCATTTTGATAT	428
Oy	442	tcacacaatccaattttttcttgtatacacctc	472
Dd	429	CAGGTTTCGAACCTTTTTCGCTGTTTCCAGTGC	459

RESULT	14	Bull6696	637 bp	mRNA	linear	EST 23-JAN-2002
LOCUS		Bull6696				
DEFINITION		Bull6696 unpublished oligo-capped cDNA library; C. elegans L1 stage				
ACCESSION		Bull6696				
VERSION		Bull6696.1				
KEYWORDS		GI:18276808				
SOURCE		Caenorhabditis elegans.				
ORGANISM		Caenorhabditis elegans.				
REFERENCE		Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				
AUTHORS		; Rhadditidae; Pelodierinae; Caenorhabditis.				
		1 (bases 1 to 637)				
		Kohara,Y., Shih-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.				
		and Sugano,S.				
TITLE		A complementary view of the C.elegans genome				
JOURNAL		Unpublished (2002)				
COMMENT		Contact: Tadasu Shih-I				
		Center For Genetic Resource Information				
		National Institute of Genetics				
		1111 Yata, Mishima, Shizuoka 411-8540, Japan				
		Tel: 81-559-81-6856				
		Fax: 81-559-81-6855				
		Email: tshih@genes.nig.ac.jp.				
FEATURES		Location/Qualifiers				
source		1..637				
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		elegans L1 stage"				
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		/dev_stage="L1"				
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Matches 96;	Conservative 0;	Mismatches 55;	Indels 0;	Gaps 0;

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Oy	382	tacaatgcagtgcagataatgcaatccgaacgtcattactatgcaagcttggatat	441
Dd	405	TACATTCGCAATTTCAGTTATGGCAGTGTATGCAGCACCGTTTATTATTCATCATTTTGATAT	464
Oy	442	tcacacaatccaattttttcttgtatacacctc	472
Dd	465	CAGGTTTCGAACCTTTTTCGCTGTTTCCAGTGC	495

RESULT	15	Bf704392	487 bp	mRNA	linear	EST 22-DEC-2000
LOCUS		Bf704392/c				
DEFINITION		MI-P-B6-acc-d-08-1-UM.s1 MI-P-E6 Sus scrofa cDNA clone				
ACCESSION		Bf704392				
VERSION		Bf704392.1				
KEYWORDS		GI:11989800				
		EST.				

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SOURCE          pig
ORGANISM        Sus scrofa
                Euarctota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
REFERENCE       1 (bases 1 to 487)
AUTHORS         Bonaldo/M.F., Lennon/G. and Soares/M.B.
TITLE           Normalization and subtraction: two approaches to facilitate gene
                discovery
JOURNAL         Genome Res. 6 (9), 791-806 (1996)
MEDLINE         97044477
COMMENT         Contact: Tuglie CK
                Molecular Genetics Laboratory, Department of Animal Science
                Iowa State University
                201 Kildee Hall, Ames, IA 50011-3150, USA
                Tel: 5152944252
                Fax: 5152942401
                Email: cktuglie@iastate.edu
                Oligo-dT track not found, Not 1 site shown in beginning of sequence
                is likely internal to the message. cDNA library Preparation: RJ
                Woods, JA Green, RS Prather S142 Animal Science Research Center,
                Department of Animal Science, University of Missouri-Columbia,
                65211 Clone distribution: clones will be available through Research
                Genetics (www.resgen.com)
                Seq primer: M13 Forward
                POLYA=No.

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        /strain="crossbreed"
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        /lab_host="DH10B (Life Technologies)"
        /note="Vector: pUT3D-Pac (Pharmacia) with a modified
        /polylinker. Site.1: Not I; Site.2: EcoRI; The MI-P-E6
        library is derived from fetus at gestational day 20. For
        a detailed description of the library from which this
        clone was derived, please visit our web site at
        http://pigst.genome.iastate.edu/.
        TAG_SEQ=None found"

BASE COUNT      146 a          99 c          91 g          150 t          1 others
ORIGIN

Query Match      6.2%; Score 62.4; DB 10; Length 487;
Best Local Similarity 60.7%; Pred. No. 0.0052;
Matches 102; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

OY 309 tgcacagaaccgaagaataatcatatgatctaatcttgtagatgagtggtgccaagaat 368
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 447 TTCCATATGAGGAAAGAAAGCTTCATATAAACAATTTTACATGCAATGTACACCAAGAT 388
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 369 taaagcgttgatcatcatgcatgcatgcatatgatgcaatccagagcatctactatgac 428
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 387 CAAAGACCTTGGAATCAACCTGCATTCACATGTGATGGCAATCAGGAACATGCTTACTACGC 328
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 429 aagcttggtatccacaatccatctttcttcgttatcacctctca 476
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 327 CAGTTTGGTTACCAATCACAAGCTTCTTTGGACGCTTCAGACCGCTTA 280
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Search completed: September 12, 2002, 08:10:22
Job time: 16652 sec
    
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 07:29:49 ; Search time 3917.59 Seconds
(without alignments)
5347.028 Million cell updates/sec

Title: US-09-508-377-10_COPY_9500_10500

Perfect score: 1001

Sequence: 1 tccgacatagacacatga.....ctggacatagctttttt 1001

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_da: *
2: gb_htg: *
3: gb_in: *
4: gb_ov: *
5: gb_ov: *
6: gb_pal: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sy: *
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13: gb_un: *
14: gb_vl: *
15: em_ba: *
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17: em_fun: *
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19: em_mu: *
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21: em_or: *
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23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	1001	100.0	11463	6	AX031271	AX031271 Sequence
2	978	97.7	11475	8	AF38431	AF38431 Aegilops
3	223.2	22.3	23449	8	AF072725	AF072725 Zea mays
4	136.4	13.6	2726	8	AF38432	AF38432 Triticum
5	136.4	13.6	2970	8	AF286319	AF286319 Triticum
6	136.4	13.6	2970	8	TASBA2	TASBA2 Triticum
7	134.8	13.5	2853	8	TA066376	TA066376 Triticum
8	130	13.0	2554	8	AF064560	AF064560 Hordeum v
9	122	12.2	2795	8	ZM065948	ZM065948 Zea mays st
10	118.8	11.9	2364	6	E14724	E14724 Rice mRNA f
11	118.8	11.9	3015	6	E14723	E14723 Rice mRNA f
12	118.8	11.9	3015	6	AB023498	AB023498 Oryza sat
13	110.8	11.1	2725	6	AR106495	AR106495 Sequence
14	110.8	11.1	2725	6	MZGLUCTRN	MZGLUCTRN
15	107.8	10.8	419	8	AF451191	AF451191 Oryza sat
16	106	10.6	2918	8	RI08CR3	RI08CR3
17	106	10.6	2919	6	E08183	E08183 Gene of Sta
18	98	9.8	2780	8	AF064561	AF064561 Hordeum v
19	95.2	9.5	2913	6	A92162	A92162 Sequence 28
20	94.8	9.5	3360	8	AB029548	AB029548 Phaseolus
21	94.2	9.4	3074	6	AR123355	AR123355 Sequence
22	93.6	9.4	2982	8	STU011888	STU011888 Solanum t
23	93.6	9.4	3003	6	A58162	A58162 Sequence 12
24	93.6	9.4	3090	6	A92164	A92164 Sequence 30
25	92.8	9.3	2529	6	A58167	A58167 Sequence 17
26	92.6	9.3	1393	6	AR123356	AR123356 Sequence
27	92	9.2	2493	6	STSBE1	STSBE1
28	92	9.2	2523	8	STU011889	STU011889 Solanum t
29	92	9.2	2955	8	STU011885	STU011885 Solanum t
30	92	9.2	2992	8	STU011890	STU011890 Solanum t
31	92	9.2	3033	6	A58164	A58164 Sequence 14
32	91.6	9.2	3549	6	PSSBERGEN	PSSBERGEN
33	90.4	9.0	2563	6	AX256072	AX256072 Sequence
34	90.4	9.0	2576	6	A58166	A58166 Sequence 16
35	90.4	9.0	2578	6	A58169	A58169 Sequence 19
36	90.4	9.0	2975	6	A58163	A58163 Sequence 13
37	90.4	9.0	3231	6	A58168	A58168 Sequence 18
38	88.6	8.9	102897	8	ATF17C15	AL162506 Arabidops
39	88.4	8.8	2517	8	AB042937	AB042937 Ipomoea b
40	88.4	8.8	3123	8	AB071286	AB071286 Ipomoea b
41	85.2	8.5	2542	8	AT022428	U22428 Arabidops
42	81.6	8.2	7020	8	ATSB21	AJ000497 Arabidops
43	81.6	8.2	101365	8	AC006919	AC006919 Arabidops
44	80.8	8.1	2668	8	ATU18817	U18817 Arabidops
45	67.4	6.7	2872	10	BC017541	BC017541 Mus muscu

ALIGNMENTS

RESULT 1
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LOCUS Sequence 10 from Patent WO9914314.
DEFINITION AX031271
ACCESSION AX031271
VERSION AX031271.1 GI:10278603
KEYWORDS
SOURCE
ORGANISM
Aegilops tauschii.
Aegilops tauschii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticaceae; Aegilops.
REFERENCE
1 (bases 1 to 11463)
Li, Z., Morell, M. and Rahman, S.
Regulation of gene expression in plants
Patent: WO 9914314-A 10 25-MAR-1999;
JOURNAL
GOODMAN FIELDER LTD (AU) ; LI ZHONGYI (AU) ; MORELL MATTHEW (AU) ;
RAHMAN SADEOUR (AU) ; UNIV AUSTRALIAN (AU) ; COMMW SCIENC INT RES
ORG (AU) ; GROUPE LIMAGRAIN PACIFIC PTY L (AU)

FEATURES
source
1..11463
Location/Qualifiers
/organism="Aegilops tauschii"
/db_xref="taxon:37682"

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 BASE COUNT 3093 a 2253 c 2422 g 3689 t
 ORIGIN

Query Match 100.0%; Score 1001; DB 6; Length 11463;
 Best Local Similarity 100.0%; Pred. No. 4.4e-208;
 Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tccgacatagacacgcatgacacatatacaagctctctcttctgacagatatagtatattca 60
 DB 9500 TCCGACATAGAACACGACATGACATATCAAGCTCTCTTGTGCAGAGATATGATGATTCA 9559
 QY 61 tggctctggaagcttcaactcttcgactgacgctgctgacgacattacataaatgat 120
 DB 9560 TGGCTCTGGATAGGCTTCAACTCTTCGCAATTCGATGCTGGCATGACATTCATTAATAATGAT 9619
 QY 121 caggctctgacacatagggtttaggtgtgtaagagctatcttaacttcaatggaatgagt 180
 DB 9620 CAGGCTTGTACACATGGGTTTAGGCGTGAAGGCTATCTTAAGCTCATGGGAATGAGATT 9679
 QY 181 tgggacatccggtgacgctcttaacaacattatgcattctgcattgattgattactgta 240
 DB 9680 TGGGACATCTCGTCACTCTTACCAACATTAATGCAATTCGATGATGATGATTTACTGTA 9739
 QY 241 attggaacacgctcttcttccacattgattgattgattgattgattgattgattgattg 300
 DB 9740 ATTGGAACACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 9799
 QY 301 gaagtttaacttcttactctgacagaaatgataatttccaaagagcccaacaactct 360
 DB 9800 GAAGTTACTCTCTAATTTACTTGGCAGAAATGATGATTTTCCAGAGGCCCAACAACCTCT 9859
 QY 361 tccaacggcgaagaagttcccccctggaaataacaatagttatgataaatagcgcgtagat 420
 DB 9860 TCCAACGGCGAAAGTTCCCTCCCTCGAAATTAACATTAATGATTAATAAGCCGCTAGAT 9919
 QY 421 ttgactcttgtaagttttagctgtgcttattacattccctactagattctttagtgcatt 480
 DB 9920 TTGACTCTTGTAAAGTTTAAAGCTGTGCTATTAATTCCTCACTAGATGATTTTATGGCCATT 9979
 QY 481 tattcttgatgaaatacaatattgtttagtgaagaatcaaatgcttctttagtatttg 540
 DB 9980 TATTCTTGATGAATCATATATGTTTGTAGAAAGATCAACATTTGTTTGTAGTTTGG 10039
 QY 541 tagacgttaacaataagtaagtgtgtgagaggtgtgtgattcaataaataatcatgattttt 600
 DB 10040 TAGACGTTTAACATTAAGTATGATGAGAGTTGTGATCATTAATAAATTCATGATTTT 10099
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 DB 10100 GCAGGGAGATCAGATTTTCTTACATATCTGTGATGCAAGAGTTCCGATCAGGCAATGCA 10159
 QY 661 gcactctgaggaataaataatgaggtatagtcactggttcttcttcttctgatacaaatgac 720
 DB 10160 GCACCTTGAGGAAAAAATATGCGGATATGCTACTGGTTTCTTTGTGCAATAAAGTAC 10219
 QY 721 agtttaacgtcagctctcttcaagtgtgtaaaaaaagttagaataatctctgttaataga 780
 DB 10220 AGTTTAACGTCAGTCTCTTCAAGTGTGTAATAAAGTATTAATTAATTCCTGTAATGAGA 10279
 QY 781 tgaataacgtgcgaaggcgagagctggaattgcttttccaaactatttcttaagtc 840
 DB 10280 TGAATAACGTGCAGGAAGGCGAGCTGGAATTCCTTTTCAACCAAACTATTTCTTAAGTGC 10339
 QY 841 ttggtatgatacatataccagacacgacacgacacgacacgacacgacacgacacgacacgac 900
 DB 10340 TTGGTATGATGATATACATATACAGACACGACACATGATGATGATGATGATGATGATGAT 10399
 QY 901 ccagatgattcaccggaataacatgagaagataaggtgatacatctcctcaaaagagagattt 960

DB 10400 CCAGATGATTTCCAGGAACATGAGAGATAGATGATCATCCCAAAAGAGAGATTT 10459
 QY 961 ggtattgcttcaactccactgagacatagcttttg 1001
 DB 10460 GGTATTGTTTCAACTTCACCTGAGCAATAGCTTTTGTG 10500

RESULT 2
 AF338431 11475 bp DNA linear PLN 27-MAR-2001
 LOCUS
 DEFINITION Aegilops tauschii starch branching enzyme Ila gene, complete cds.
 ACCESSION AF338431
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Aegilops tauschii.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Aegilops.
 1 (bases 1 to 11475)
 Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,
 Kosar-Hashemi, B., Abrahams, S. and Morell, M.K.
 Comparison of Starch-Branched Enzyme Genes Reveals Evolutionary
 Relationships Among Isoforms. Characterization of a Gene for
 Starch-Branched Enzyme Ila from the Wheat D Genome Donor Aegilops
 tauschii
 Plant Physiol. 125 (3), 1314-1324 (2001)
 MEDLINE 21140316
 PUBMED 11244112
 REFERENCE
 2 (bases 1 to 11475)
 Rahman, S., Regina, A., Li, Z., Sharon, A. and Morell, M.K.
 Direct Submission
 Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,
 Canberra, ACT 2601, Australia

FEATURES
 Source
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 location/Qualifiers
 /organism="Aegilops tauschii"
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 /db_xref="GI:13447950"

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 EYKRIARAIDOHGGGLEAPSRGVEKLGKPSAEGITRYREMAPAQAHSALVGDPMNP
 NADMTRDDGVWEIPLPNADSSALPHGSRKATRDPTSGKDSISANIKSVQAP
 GEIPFNGIYVDPPEEEKYVFOHQRKPESLRIYESHIGMSSEPKINSVAFNRDEVL
 PRKIRGYNAVQIMAIQDEHSYVASFQVHVPFAPSSRFETPEDLSLIDRAHELGL
 VLMDIYHSSNNMTLDGFDGDFEYFPGGPRGHMMDSRLFNFGSVEVLFLLS
 NAWWMLSEYKDFGPRDGYSMAVTHHGLQMTFGNGVEFGRATDVAVYLVAVND
 LIHGLPDAVSTEDVSGMPTFCIPVDDGVGFDYRIHMAVADKWLIELKQSPESKMK
 GDIVHTLTNRMLKECVYTAESHQALVGGTILAFVLMDDMTDFMALVPLRSTLRDK
 GIALHKMIRLVMTLGEGEYLAESHQALVGGTILAFVLMDDMTDFMALVPLRSTLRDK
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 BASE COUNT 3093 a 2253 c 2423 g 3689 t 11 others
 ORIGIN

polYA_signal /gene="ae"
19843. .19849
polYA_site /gene="ae"
19879
BASE COUNT 6409 a 4892 c 4904 g 7244 t
ORIGIN

Query Match 22.3%; Score 223.2; DB 8; Length 23449;
Best Local Similarity 58.6%; Pred. No. 7,7e-39;
Matches 649; Conservative 0; Mismatches 333; Indels 126; Gaps 10;

QY 19 gaacatacaagctctcttctgagagatagtatgattcattgctcctgataagg-ctt 77
DB 17812 GAACCTCAGCTGCTCTTATATGAGAGATATGATGATTCATGAGCCCTGATGAGACTT 17871
QY 78 caactctgcattgacgagcgaacgaacattacataaagatcgaagcttgccatg 137
DB 17872 CAACCTCAGCTGCTCTTATATGAGAGATATGATGATTCATGAGCCCTGATGAGACTT 17931
QY 138 gtttaagtggtgaagcctccttactcattggaagattggtgcatccctgctcaat 197
DB 17932 GTTAAAGAGAGAGAGGCTATCTTATATTCATGGAATGAGTTGGACATCCTGCTGAGA 17991
QY 198 cttacaacattatgcatctcgaatgattgattcattgtaa-----ttgaac 248
DB 17992 TTTAACTACTGTTGTTTATTAACCTTCGTTGAGCTTTATATGACAGTACCTCATCCAAC 18051
QY 249 catgcttctcttcaacttgatgattatgtaatacctgctgctcccaagagaagatlaa 308
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QY 309 ctctattacttgagcaaatgataatttcccaagagcccaaccccttccaaacg 368
DB 18112 CTCTCTATTTATTTTGGCAATGATGATTTTCCAAAGAGCCGCAAAAGATTTCCAAAGTG 18171
QY 369 gcaagctctccctcggaataaacaatagatgataaagccgctagattgactt 428
DB 18172 GT-AGTTTATTCAGGAGATTAACAAAGATGACAAAGTGCCTGCAAGATTGACCTG 18230
QY 429 gtaagtttagcgtgctgattacatccctcactagactcttattgcca----- 478
DB 18231 GTAAACTCTCTTGTGATGTTGCAAAAAGTTCAAAGTTGATTTACTTTTACACATGATCCAG 18290
QY 479 -----ttattcttgatgaatacaatgattg 507
DB 18291 TGCCTTAAATGACAGAGTGCATTTATATAGTCTCTTATTCATATTTAGCATGTTCC 18350
QY 508 ttgaggaagatcaaatgcttctgtt--agttttagaacgttaacataagtagtg 565
DB 18351 AGAAGTAAATAATTTACTACTCTTGTAAAGTTTCTTATATATATGCTGCTTGTGG 18410
QY 566 agagtggttcatcatttaaaatcatgattttt-----gagggagatgcagatt 618
DB 18411 TCATATAATTCGATATATCGGAATTTGTTATTTTATTCATTGTCAGGGTGCAGACTA 18470
QY 619 tcttagatcagtggtatgaagattcgaacgaacatcagcatcttgaggaataa 678
DB 18471 TCTTAGTATCATGCTATGCAAGAGTTTGCATGCGCAATGCACATCTTGACGCAAAAATA 18530
QY 679 ttgggagatg-----tcaactggttctcttcttgatcaataaagtcacagtt 725
DB 18531 TGAAGTATGTTCTTTTACTTTTATCTTTTGTGATTTGGTCTGCAAGGTTTCACAAACATCAT 18590
QY 726 aagtcagctctctcaagtggttaaaaaagtgtagaattatccctg-----taatg 777
DB 18591 AATTTGTTGTCATCTTACTCTTGTATATGTCATTTTAAAAAATCATCTTCCTCAGTTTATCTG 18650
QY 778 agatgaaacatgctgcaaaagcgagctggaattgct-----ttcaccaaacattttc 832
DB 18651 AGCTTTTAAACATGAAAGGTTTCAATTTATGAATCTTTCAATGTCATCAACAACTTTAG 18710

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DB 18711 GTATTTTCATGATCATTAATAAGTACTCTGGAGACAGCAGCCCATATGTAAGCAAAAT 18770
QY 854 catalaccagactgcaaaatgactcattttagcactctgagccagctatgttca 913
DB 18771 TTTCTGATGAATTTGCTGTGATATTCAGTCTGATGACATCTGATCCAGATATATTTCC 18830
QY 914 cggaaacatgaaggaagatgaagctatccctcaaaagagagattgatttcttc 973
DB 18831 CGGAACATGAGAGAGATTAAGGATGCTGTTGCAAAAAGAGAGATTGATTTGCTGTC 18890
QY 974 aactccactggaagcaatgaactttttg 1001
DB 18891 AACTTCCATGCAACACAGCTATTTTG 18918
RESULT 4
AF338432
LOCUS 2726 bp mRNA linear PLN 27-MAR-2001
DEFINITION
Triticum aestivum starch branching enzyme I1a variant mRNA,
complete cds.
ACCESSION
AF338432.1 GI:13447951
VERSION
AF338432.1
KEYWORDS
broad wheat.
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 2726)
REFERENCE
Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,
Kosar-Hashemi, B., Abrahams, S. and Morell, M.K.
Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary
Relationships Among Isoforms. Characterization of a Gene for
Starch-Branching Enzyme I1a from the wheat D Genome Donor Aeqllops
tauschii
JOURNAL
Plant Physiol. 125 (3), 1314-1324 (2001)
MEDLINE
21140316
PUBMED
11244112
REFERENCE
2 (bases 1 to 2726)
AUTHORS
Rahman, S., Regina, A., Li, Z., Abrahams, S. and Morell, M.K.
TITLE
Direct Submission
JOURNAL
Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,
Canberra, ACT 2601, Australia
FEATURES
source
1..2726
Location/Qualifiers
/organism="Triticum aestivum"
/db_xref="taxon:4565"
124..2430
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DENNMNPADMTMDYGYWEITFIPNNAGSALIPDGVSFVRLHMAVADKMIELAKO
KESVQAPGEIPNGIYDPPPEEKYFQAPORRPSLTIYESHIGMSSPERKINSYA
NFRDEVLPIKRIKRIYNAVQIMAIQESHYTAQFVHTNFPASRSRGTEDEKLSLDR
AHEGLILVMDIVSHSSNNTLDGLMFGDTGTHYFHGGPRGHMMWDSRLFNYSWE
VIRFLISNARWMLLEEKFDGFRPDGVTGVTNHNHGLQMTFNGVGEFADVDVAIV
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SPESKMGDIIVHTIRNRRLERKCVFAESHDQALVGDKITAFIMDKMDYDPMALDRP
STPRIDRGIALKRIKRIYTMIGAGEYILNFMNGENRHPWIDPFRGPTLPKYILPG
NNNSIDKCRRRFDLGDADFLRTIHGMQEFDAQIHLEKTFGWTSEHQTIVSKHEDKY
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BASE COUNT 726 a 564 c 701 g 735 t
ORIGIN

Query Match 13.6%; Score 136.4; DB 8; Length 2726;
Best Local Similarity 98.7%; Pred. No. 8.3e-20;
Matches 148; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 43 aggatgtatgatttcattcagctctgagatagg-cttcaactcttcgcatgacgttgaca 101
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DB 1787 AGGATGTATGATGATTTCATGCGCTCTGGATAGGCGCTCAACTCCTCGCATGTATCGTGCA 1846
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QY 102 tagcatataataaataatgacagcttgtaaccatggtttaggttgtagaagctactcta 161
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DB 1847 TAGCATTAACATAAATGATCAGGCTTGTCACCATGGGTTAGGTGATGAAGGCTATCTTTA 1906
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QY 162 actcatgggaaatgagtttg9gacccctg 191
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DB 1907 ACTTCATGGGAATGAGTTGGGCATCCTG 1936
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RESULT 5
AF286319 2970 bp mRNA linear PLN 30-OCT-2000
LOCUS Triticum aestivum starch branching enzyme 2 (Sbe2) mRNA, complete
DEFINITION cds
ACCESSION AF286319
VERSION AF286319.1 GI:11037533
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 2970)
McCue,K.F., Hurkman,W.J., Tanaka,C.K. and Anderson,O.D.
Starch Branching Enzymes Sbe1 and Sbe2 from Wheat (Triticum
aestivum cv. Cheyenne): Molecular Characterization, Developmental
Expression, and Homolog Assignment by Differential PCR
Unpublished
2 (bases 1 to 2970)
McCue,K.F. and Anderson,O.D.
Direct Submission
Submitted (11-JUL-2000) United States Department of Agriculture,
Agricultural Research Service, 800 Buchanan Street, Albany, CA
94710-1105, USA

FEATURES
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Location/Qualifiers
/organism="Triticum aestivum"
/cultivar="Cheyenne"
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149..2620
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alpha-1,4-glucan-6-glucosyltransferase"
/codon_start=1
/product="starch branching enzyme 2"
/protein_id="AAC27623.1"
/db_xref="GI:11037534"

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DEVLPRIKRLGNAVAQIMAIQESHYSYASFGYHVNFPAPSSRGTPEDLKSLINAFH
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BRGLDVFVFNHMSNPFEDYRGCSRPCKYKVALDSDALFEGFSRLDHDVYFTTEH

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BASE COUNT 775 a 643 c 774 g 778 t
ORIGIN

Query Match 13.6%; Score 136.4; DB 8; Length 2970;
Best Local Similarity 98.7%; Pred. No. 8.2e-20;
Matches 148; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 102 tagcatataataaataatgacagcttgtaaccatggtttaggttgtagaagctactcta 161
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DB 2037 TAGCATTAACATAAATGATCAGGCTTGTCACCATGGGTTAGGTGATGAAGGCTATCTTTA 2096
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QY 162 actcatgggaaatgagtttg9gacccctg 191
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DB 2097 ACTTCATGGGAATGAGTTGGGCATCCTG 2126
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RESULT 6
TASBA2
LOCUS TASBA2
DEFINITION T.aestivum mRNA for starch branching enzyme II.
ACCESSION Y11282
VERSION Y11282.1 GI:1885343
KEYWORDS
1,4-alpha-glucan branching enzyme; sbe2 gene; starch branching
enzyme II.
SOURCE
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 2970)
Nair,R.B., Baga,M., Scoles,G.J., Kartha,K.K. and Chibbar,R.N.
Isolation, characterization and expression analysis of a starch
branching enzyme II cDNA from wheat
Plant Sci. In press
2 (bases 1 to 2970)
Chibbar,R.N.
Direct Submission
Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology
Institute, National Research Council of Canada, 110 Gymnasium
Place, Saskatoon, Saskatchewan S7N 0W9, CANADA

FEATURES
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/organism="Triticum aestivum"
/cultivar="Fielder"
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151..312
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151..2622
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/db_xref="GI:1885344"

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NMNPAADMTDDYGVWEITFLPNNDGSPALPHGSRVIRIMDTSPGVDISAWTKFS
VOAPEIFPNCIYDPPPEEKYVFOHPQPKPRESLRITESHIGMSSPEKINSANFR
DEVLPRIKRLGNAVAQIMAIQESHYSYASFGYHVNFPAPSSRGTPEDLKSLINAFH
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LVNDLILHGLHPDASIGEDVSGMPTFCIPVDDGVGLDYRLHMAVADAKWIELLKQSE
SMKMGDIYVHTLTNRMRLEKCYTAESHDAALVGDKTIAFMLMDMTDFMALDRPSTP
RIDRIGIALHKMIRLVITMGLGEGYLANFMENFGEHPIDEPRGPOTLPTGVLPLGNNN
SYDCRRRFDLGDADFLRYHGMQFDOAMOLEEKYGMPTSEHOYVSRKHEDVYLIE
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2930..2935
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2948
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ORIGIN

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Best Local Similarity 98.7%; Pred. No. 8.2e-20;
Matches 148; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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Db 1979 AGGATATGTATGATTTTCATGCGCTCGATAGGCGCTTCAACTCCCTGCATGTATGCTGGCA 2038
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QY 102 tagcaatcacaataatgacagctctgacacatgggttgatggatgagatgacatctta 161
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Db 2039 TAGCATTTACATTAATAATGATCAGGCTTGTCACCATGGCTTGTAGTGGTGAAGCTATCTTA 2098
|||||
QY 162 actcatggaatgagttggcagctcctg 191
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Db 2099 ACTTCATGGGAATGAGTTTGGCATCTCTG 2128
|||||

RESULT 7
TAU66376 2853 bp mRNA linear PLN 18-OCT-1996
LOCUS
DEFINITION Triticum aestivum 1,4-alpha-D-glucan
6-alpha-D-(1,4-alpha-D-glucanotransferase mRNA, complete cds.
U66376
U66376.1 GI:1620661
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum
wheat.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 2853)
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (08-AUG-1996) University of Hamburg, Institute of General
Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr.
18, Hamburg 22609, Germany
location/Qualifiers
1..2853
/organism="Triticum aestivum"
/cultivar="T.A. Florida"
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/tissue_type="kernels 21 DAP"
313..2502
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/note="branching enzyme"
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6-alpha-D-(1,4-alpha-D-glucanotransferase"
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PGGQKRIYEIDPLKDRSHLDYRKYRKIRRAIDQHEGGLFAFSGYKELGFTTNSA

EGTIRKMAHGAHSAALVGPNNMNPADAMTRDDYCYWELFLPNNADGSSALPHGSR
VKIRMDTPSSVKKOSISAWIKFSVQAPBEIPFNGITYDPPEEKIVFQHPKRPESLR
IYESHIIOMSSPEPERINSYANFROVEYLRIRKRGINAVOIAIOESHYSAGFYHYNF
FASSRHGTEDEDLKSLIDRAHEGLGLVLMIDIVSHSSNNTLDGLNGFDGDTTHYFHG
PRGHMMWDRLEFNGSWEYVRLFLSNARWMLLEKYNFDFRFGVTSMTYTHHGLQMT
FTNGYGEYFGRATDVAVYILMVLNDLILHGLPDAVIGEDVSGMPTFCIPVDDGVG
PDYRLHMAVADAKWIELLKQSEBKRMDIYHTLTNRMRLEKCYTAESHDAALVGDKT
IAFMLMDMTDFMALDRPSTPRIDRIGIALHKMIRLVITMGLGEGYLANFMENFGEHPI
WIDFPRGPOTLPTGKVLPGNNNNYDKCRRRFDLGDADFLRYRGQFDOAMOLEEKY
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BASE COUNT 776 a 585 c 746 g 746 t
ORIGIN
Query Match 13.5%; Score 134.8; DB 8; Length 2853;
Best Local Similarity 98.0%; Pred. No. 1.8e-19;
Matches 147; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Db 1859 AGGATATGTATGATTTTCATGCGCTCGATAGGCGCTTCAACTCCCTGCATGTATGCTGGCA 1918
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QY 102 tagcaatcacaataatgacagctctgacacatgggttgatggatgagatgacatctta 161
|||||
Db 1919 TAGCATTTACATTAATAATGATCAGGCTTGTCACCATGGCTTGTAGTGGTGAAGCTATCTTA 1978
|||||
QY 162 actcatggaatgagttggcagctcctg 191
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Db 1979 ACTTCATGGGAATGAGTTTGGCATCTCTG 2008
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RESULT 8
AF064560 2554 bp mRNA linear PLN 03-NOV-1998
LOCUS
DEFINITION Hordeum vulgare Bomi Starch branching enzyme IIA (sbeIIa)
mRNA, nuclear gene encoding plastid protein, complete cds.
AF064560
AF064560.1 GI:3822019
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare
barley.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 2554)
REFERENCE
AUTHORS
TITLE
JOURNAL
Sun C., Sathish P., Ahlandsberg S. and Jansson C.
The two genes encoding starch-branching enzymes IIA and IIB are
differentially expressed in barley
Plant Physiol. 118 (1), 37-49 (1998)
98404232
REFERENCE
AUTHORS
TITLE
JOURNAL
Sun C., Sathish P., Ahlandsberg S. and Jansson C.
Direct Submission
Submitted (11-MAY-1998) Stockholm University, Biochemistry,
Stockholm S-10691, Sweden
location/Qualifiers
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QVVPKRDGCKRITIDPTLKDPRSHLDYRKYRKIRRAIDQHEGGLFAFSGYKELGFTTNSA

FTSAKITYREMAFGAHSALVGDPMNNMNPADMTDRDXYGWEIEFLPNADGSPAI
PHGRVIRMTDPTSGVKDSISAMTKESVQACETIPNCTIYDPRPEEKEYVQHOPRK
PESLRVIESHTGMSPEPKINSYANFEDVLPRIKLGYNVQIMAOEHSYVASFQ
HVNTEPASHREFTPEDEKSLIDRAHEGLVIMDIYHSHSNNTLGLNFDSDTH
YFHGPRHMMMSRLEFNVSWEVRLISNARWLEVEYKFDEGRFEDGYVSMYTH
GLOMTEFNAGEYGFATVDVAVYLMVNDLIGLVDAYSIGEDVSGMPTFCIPV
DGGVFDYRLHMAVADKIELLKOSDSMKKGDIVHTLNRMLKCYTVASHDOAL
VGDKTIAFWLMDKMDYMDALDRSPTRIDGIALHKIRLVTMGLGEGTLNMGNE
FGHPWIDFPRGPOTLPTGKYLPGNNNSYDKCRFRFDGADFLRYRMQFEDAMOH
LAEKYSFMSHSHQVSRKHEDKYLIFERGLVVFENHWSNKKDVRVGSCKGKX
VLESDYDMLFEFGSRLDHVDYFTTEHHDNRPRSFSYTPESRTAVVYALTE"

BASE COUNT 731 a 494 c 632 g 697 t

ORIGIN

Query Match 13.0%; Score 130; DB 8; Length 2554;
Best Local Similarity 96.0%; Pred. No. 2.1e-18;
Matches 144; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 43 aggaatgataattcattcgtcgtcgtgtag-gctcaacttcgtcattgacgtgca 101
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Db 1568 AGGATATGATGATTTTCATGCTCTGGATAGACCTTCAACCCCTGCATTGATCGGGCA 1627
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Qy 102 tagcatataaataatgacagctgtcaccatggttagtggtgaagcatctta 161
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Db 1628 TAGCATTCATTAATAATGATCAGCTTGTCACCATGGGTTAGTGGCGAAGCTATCTTA 1687
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Qy 162 actcataggaatagattggcactctg 191
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Db 1688 ATTCATGGGAATGAGTTGGGCATCCG 1717
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RESULT 9
LOCUS 2M065948 2795 bp mRNA linear PLN 21-AUG-1997
DEFINITION Zea mays starch branching enzyme IIA (Sbe2a) mRNA, partial cds.
ACCESSION U65948
VERSION U65948.1 GI:2340107
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 2795)
AUTHORS Gao,M., Fisher,D.K., Kim,K.N., Shannon,J.C. and Guiltinan,M.J.
TITLE Independent genetic control of maize starch-branching enzymes IIA
and IIB. Isolation and characterization of a Sbe2a cDNA
JOURNAL Plant Physiol. 114 (1), 69-78 (1997)
MEDLINE 97303618
REFERENCE 2 (bases 1 to 2795)
AUTHORS Gao,M., Fisher,D.K., Kim,K.-N., Shannon,J.C. and Guiltinan,M.J.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1996) Hort.,Biotech.Inst., Penn State University,
519 Wartik, University Park, PA 16802, USA
FEATURES
source Location/Qualifiers
1. 2795
/organism="Zea mays"
/strain="B73"
/db_xref="taxon:4577"
/note="indred"
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/gene="Sbe2a"
<1..2446
/gene="Sbe2a"
/EC_number="2.4.1.18"
/function="formation of alpha-1-6 glucosidic linkage in
starch biosynthesis"
/note="starch branching enzyme isozyme SBEIIa"
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/db_xref="GI:2340108"

/translation="DLPSEVLRFRKDAEPRVTLSCAGAPGVLPVGGSDLLSSABPV
VTPPEBEQIPEALVYTEKTSSTPTQTTSAVAEASSVSEAEERPELSEVIGVGTGCT
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DQHGAGDAEPRGEEKLGEFTSAAGIYREMAAPAYSAALVGGDPMNNPNADAAARE
YGVMEIFLPNNADGSPAIPHGRVRIEMDTPSGKDSIPAAIKFSVOAPRIPYNGIY
YDPEEKEYVYKHOPKPKSLRIYESHSGMSPEPKINTYANRDEVLPRIKLGYN
AVOIMAOEHSYVAFYHVNFPASRRPCTPEDILSKDAHEGLVIMDIYHSH
SSNNTLGLNFDSDTHHYHPRGGRHMMMSRLFNYSMEVRLISNARWLEVEY
KFDEGRDGVTSMTTHHGLVITGTGTFGATVDVAVYLMVNDLIGLTPEA
VSIQEDVSGMPTFCIPVODGGVGDYRLHMAVDPKWLILKQSDYEMGDIVHTLN
RRMLEKCYTVCESHDOALVGDKTIAFIMLMDKMDYMDALDRSPTRIDGIALHKMR
LVTMGLGEGTLNMGNEFGHPEWIDFPRGGSVLPNGSVIIPGNNNSYDKCRFRDLDG
ADLYRYGMOEFDAMOHLEGEYEFEMTSDHSYGRKHEDKYLIFERGLDVFVFNPMH
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PSRTAVYIAPGAEDE"

BASE COUNT 766 a 563 c 709 g 757 t

ORIGIN

Query Match 12.2%; Score 122; DB 8; Length 2795;
Best Local Similarity 92.7%; Pred. No. 1.1e-16;
Matches 139; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 43 aggaatgataattcattcgtcgtcgtgtag-gctcaacttcgtcattgacgtgca 101
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Db 1791 AGGATATGATGATTTTCATGCTCTGGACAGGCTTCAACGCCCTGCATCGATCGGGCA 1850
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Qy 102 tagcatataaataatgacagctgtcaccatggttagtggtgaagcatctta 161
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Db 1851 TAGCATTCATTAATAATGATCAGCTTGTCACCAATGGGTTAGGAGGTGAAGCTATCTTA 1910
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Qy 162 actcataggaatagattggcactctg 191
|||||
Db 1911 ATTCATGGGAATGAGTTGGGCATCCG 1940
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RESULT 10
LOCUS E14724 2364 bp DNA linear PAT 28-JUL-1999
DEFINITION Rice mRNA for branching enzyme-4 mature peptide.
ACCESSION E14724
VERSION E14724.1 GI:5709407
KEYWORDS JP 1998004970-A/2.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 2364)
AUTHORS Baba,T., Kawasaki,T. and Ichikawa,N.
TITLE NEW RICE GENE FOR STARCH-BRANCHING ENZYME
JOURNAL Patent: JP 1998004970-A 2 13-JAN-1998;
MITSUI GYOSAI SHOKUDUTSU BIO KENYUSHO:KK, MITSUI PETROCHEM IND LTD
Oryza sativa (rice)
PC (12N5/10,C12R1:91), (C12N9/10,C12R1:19);
PN JP 1998004970-A/2
PD 13-JAN-1998
PE 24-JUN-1996 JP 1996162983
PI BABA TADASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC
C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/10, (C12N15/09, PC
C12R1:91),
PC (C12N5/10,C12R1:91), (C12N9/10,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH key Location/Qualifiers
FH source 1..2364
/organism="Oryza sativa"
/cultivar="Nihonbare"
/clone_lib="Rise Immature Seed Lambda gIII FT
CDNA library"
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/clone="pRBA1"
FT mat_peptide 1..2364

FEATURES FT /product='branching enzyme-4'.
source 1. .2364 /location/Qualifiers
/db_xref='taxon:4530'
BASE COUNT 670 a 454 c 600 g 640 t
ORIGIN

Query Match 11.9%; Score 118.8; DB 6; Length 2364;
Best Local Similarity 91.3%; Pred. No. 5.7e-16;
Matches 137; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 43 aggatatgatattcattcagctctgtagatg-gcttaactcttcgattgtagcga 101
|||||
Db 1721 AGGATATGATGATTTATGAGCTGTACACAGACCTTCAACACCGCATGATGATGGA 1780
|||||

QY 102 tagcattacaataaataagcagctgtcaccatgggttagtgtaggaagcattccta 161
|||||
Db 1781 TAGCATTACATTAATAATGATGAGCTGTACACAGGCGGAGGAGGAGGATCTTA 1840
|||||

QY 162 acttcattgggaatgagttcgggcatcctg 191
|||||
Db 1841 ATTTCATGGGAATGAGTTGGGCATCCTG 1870
|||||

RESULT 11
LOCUS E14723 3015 bp DNA linear PAT 28-JUL-1999
DEFINITION Rice mRNA for branching enzyme-4, complete cds.
ACCESSION E14723
VERSION E14723.1 GI:5709406
KEYWORDS JP 1998004970-A/1.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 3015)
Baba,T., Kawasaki,T. and Ichikawa,N.
NEW RICE GENE FOR STARCH-BRANCHING ENZYME
Patent: JP 1998004970-A 1 13-JAN-1998;
MITSUI GIOSAI SHOKUBUTSU BIO KENKYUSHO:KK, MITSUI PETROCHEM IND LTD
OS Oryza sativa (rice)
PN JP 1998004970-A/1
PD 13-JAN-1998
PI 24-JUN-1996 JP 1996162983
PT BABA TADASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC
C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/10,C12N15/09, PC
C12R1:91),
PC (C12N5/10,C12R1:91),(C12N9/10,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key
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FT source 1. .3015
FT /organism='Oryza sativa'
FT /cultivar='Nihonbare'
FT /clone_lib='Rice Immature Seed Lambda gIII FT
FT CDNA library'
FT /tissue_type='Immature seed'
FT /clone='pRB41'
FT CDS 129. .2654
/product='branching enzyme-4' FT sig_peptide

FEATURES
source 1. .3015
location/Qualifiers
1. .3015
/organism='Oryza sativa'
/db_xref='taxon:4530'
BASE COUNT 796 a 606 c 819 g 794 t
ORIGIN

Query Match 11.9%; Score 118.8; DB 6; Length 3015;
Best Local Similarity 91.3%; Pred. No. 5.5e-16;
Matches 137; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 43 aggatatgatattcattcagctctgtagatg-gcttaactcttcgattgtagcga 101
|||||
Db 2008 AGGATATGATGATTTATGAGCTGTACACAGACCTTCAACACCGCATGATGAGGA 2067
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QY 102 tagcattacaataaataagcagctgtcaccatgggttagtgtaggaagcattccta 161
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Db 2068 TAGCATTACATTAATAATGAGCTGTACACAGGCGGAGGAGGAGGATCTTA 2127
|||||

QY 162 acttcattgggaatgagttcgggcatcctg 191
|||||
Db 2128 ATTTCATGGGAATGAGTTGGGCATCCTG 2157
|||||

RESULT 12
LOCUS AB023498 3015 bp mRNA linear PLN 04-AUG-1999
DEFINITION Oryza sativa mRNA for starch branching enzyme rbe4, complete cds.
ACCESSION AB023498
VERSION AB023498.1 GI:5689137
KEYWORDS starch branching enzyme rbe4.
SOURCE Oryza sativa tissue library:developing seeds cDNA to mRNA.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (sites)
Mizuno,K., Tachibana,M., Kobayashi,E., Kawasaki,T., Funane,K.,
Kobayashi,M. and Baba,T.
Molecular cloning and expression analysis of a novel member of
starch branching enzyme isoform in developing rice seeds
Unpublished (1999)
2 (bases 1 to 3015)
Mizuno,K. and Baba,T.
Direct Submission
Submitted (09-FEB-1999) Kouichi Mizuno, University of Tsukuba,
Institute of Agricultural and Forest Engineering; 1-1-1 Tennoudai,
Tsukuba, Ibaraki 305-8572, Japan
(E-mail:koumomo@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-4656,
Fax:81-298-53-2203)

FEATURES
source 1. .3015
location/Qualifiers
1. .3015
/organism='Oryza sativa'
/db_xref='taxon:4530'
/tissue_lib='developing seeds'
129. .2654
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129. .2654
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/protein_id='BA82828.1'
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SFSGVYVSCAGAGKALVPGGSDLLSSAPVEVPEOPEESQIPDDMKVRFEEDE
EIPAVAEASIKVVAEDKLESEVIODIEEVENGTGKADPEVEKPRVIEPPDGO
KIYDIPMLIEGFNNHLDVRYSEVKRRAAIDOHGGGLDAPFSEKELGFRSAGITV
REMAPGAGSAAALVGDPENNNNPNADVTMTREYGVSESLIPNAGSGPATIRGSGVRLM
DTPSGVKDSIPAWIKFAVDAPCEIPIYNGIYIDPEEKEVYFQHPQKRRNSLRITFSH
IGMSSEPKINTYANFRDVLPRIKRLGNAVOIMAIQHSYVASFGYHVTNEFAS
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WMDSDRLFNYSGWSEVLRILSNARKWMLLEEKFGGFFPDGVTSMYTHGLQVAFGTNY
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HNAVPRKATIELLKQSDPEYKMGDIYATLTINRRSEKCYAAESHDALAGDGTIAFML
MCKDMTDFMALDPSPTPRIDRGIALHKMLRLVTMGIGSGYLNFNGENFGHPWIDFP
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BASE COUNT 796 a 606 c 819 g 794 t
ORIGIN

Query Match 11.9%; Score 118.8; DB 8; Length 3015;
 Best Local Similarity 91.3%; Pred. No. 5.5e-16;
 Matches 137; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

OY 43 aggatattgatattcattcagctctgtagatag-gcttcaactcttcgcatgtagcgta 101
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 DB 2008 AGGATATGTAATGATTATTAAGCGCTTAGACAGACCTTCAACACTCGCATGATCGTGGGA 2067
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OY 102 tagcatatcataaaatgtagcagctgtgtcaccatgggttaggttgtagaaggtactctta 161
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 DB 2068 TAGCATTAACATAAATGATTAGGCTTGTCACCATGGGCTTAGAGGCGAAGGCTATCTTA 2127
 |||||

OY 162 acttcatgggaatgagttgggcatccg 191
 |||||
 DB 2128 ATTTCATGGGAATGAGTTGGCATCCG 2157
 |||||

RESULT 13
 ARI06495 2725 bp DNA linear PAT 14-FEB-2001
 LOCUS ARI06495 2725 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 14 from patent US 6107060.
 ACCESSION ARI06495
 VERSION ARI06495.1 GI:12821025
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2725)
 AUTHORS Keeling, P. and Guan, H.
 TITLE Starch encapsulation
 JOURNAL Patent: US 6107060-A 14 22-AUG-2000;
 FEATURES
 source Location/Qualifiers
 BASE COUNT 727 a 534 c 715 g 749 t
 ORIGIN

Query Match 11.1%; Score 110.8; DB 6; Length 2725;
 Best Local Similarity 88.0%; Pred. No. 3.1e-14;
 Matches 132; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

OY 43 aggatattgatattcattcagctctgtagatag-gcttcaactcttcgcatgtagcgta 101
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 DB 1847 AGGATATGTAATGATTATTAAGCGCTTAGACAGACCTTCAACACTCGCATGATCGTGGGA 1906
 |||||

OY 102 tagcatatcataaaatgtagcagctgtgtcaccatgggttaggttgtagaaggtactctta 161
 |||||
 DB 1907 TAGCATTAACATAAATGATTAGGCTTGTCACCATGGGCTTAGAGGCGAAGGCTATCTTA 1966
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OY 162 acttcatgggaatgagttgggcatccg 191
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 DB 1967 ATTTCATGGGAATGAGTTGGCATCCG 1996
 |||||

RESULT 14
 MZEGUOCTRN 2725 bp mRNA linear PLN 01-JUN-1994
 LOCUS MZEGUOCTRN 2725 bp mRNA linear PLN 01-JUN-1994
 DEFINITION Corn starch branching enzyme II mRNA, complete cds.
 ACCESSION L08065
 VERSION L08065.1 GI:168482
 KEYWORDS 1,4-alpha-glucan branching enzyme; amylo-transglucosylase;
 glucanotransferase; starch branching enzyme II.
 SOURCE Zea mays cDNA to mRNA.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 2725)
 AUTHORS Fisher, D.K., Boyer, C.D. and Hannah, L.C.
 TITLE Starch branching enzyme II from maize endosperm

JOURNAL Plant Physiol. 102, 1045-1046 (1993)
 MEDLINE 94105320
 FEATURES
 source Location/Qualifiers
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 91..264
 91..2490
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 /protein_id="AAA18571.1"
 /db_xref="GI:168483"
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 ADGTSPIPHGSRVVRKMRDIPSGIKDSIPAMITYSVQAREIYDGIYYDPREYVYV
 RHAQPKRPSKLRIVETHVGMSSPEPRINTVYRDEVLPRIKLSTNAVQIMATDEHS
 YYSGCYHVTNFAPSSRGTPEDEKSLIDRAHEGLGLVMDVSHASSNTLDGLNG
 FGDGTHYFHSQPRGHMMMDRLFNYGMEVLRFLLSNARMMLLEXYKDFGRPDGVT
 SMATYHNGLOVTFGTGNENYFGEATDVDAVVYVLMVNDLHGLYPEAVTIGEDVGMP
 TPALPVHOGVGVDFRMHMAVADKMTIDLKOSDETMMKMDIYHTLJNRRMLEKCYTA
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 LNFNGNERFGHPWIDFPRGPORLPFGKFTPGNNNSYDKCRFRFDLGADVLYRHMOE
 FDOAMQHLQOKYEFMTSDHQYISRKHEEDKVIYFPERGDLVFEVFNHCNNSYFDYRIGC
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mat_peptide 265..2487
 /product="starch branching enzyme II"

BASE COUNT 727 a 534 c 715 g 749 t
 ORIGIN

Query Match 11.1%; Score 110.8; DB 8; Length 2725;
 Best Local Similarity 88.0%; Pred. No. 3.1e-14;
 Matches 132; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

OY 43 aggatattgatattcattcagctctgtagatag-gcttcaactcttcgcatgtagcgta 101
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 DB 1847 AGGATATGTAATGATTATTAAGCGCTTAGACAGACCTTCAACACTCGCATGATCGTGGGA 1906
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OY 102 tagcatatcataaaatgtagcagctgtgtcaccatgggttaggttgtagaaggtactctta 161
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 DB 1907 TAGCATTAACATAAATGATTAGGCTTGTCACCATGGGCTTAGAGGCGAAGGCTATCTTA 1966
 |||||

OY 162 acttcatgggaatgagttgggcatccg 191
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 DB 1967 ATTTCATGGGAATGAGTTGGCATCCG 1996
 |||||

RESULT 15
 AF451191 419 bp mRNA linear PLN 18-DEC-2001
 LOCUS AF451191 419 bp mRNA linear PLN 18-DEC-2001
 DEFINITION Oryza sativa granule-bound starch synthase mRNA, partial cds.
 ACCESSION AF451191
 VERSION AF451191.1 GI:17902268
 KEYWORDS
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoideae; Oryza.
 REFERENCE 1 (bases 1 to 419)
 AUTHORS Lee, D.-S. and Hur, Y.
 TITLE Expression and regulation of genes involved in carbohydrate
 metabolism in rice
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 419)
 AUTHORS Lee, D.-S. and Hur, Y.

TITLE Direct Submission
JOURNAL Submitted (23-NOV-2001) Biology, Chungnam National University, 220
Kungdong, Yuseong-Ku, Taejeon 365-764, Korea

FEATURES
Source location/Qualifiers

1. .419
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/cultivar="Stejaree45"
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/protein_id="AAL47851.1"
/db_xref="GI:17902269"
/translation="LYPEAVAIGEDVSGMPFCIPVODGVGFDRLLHMAVPDKWIGL
LKODEYWKMGDIYHTLTNRMSKCVYAESHOALVGDXTIAFWLMDKMDYDMAL
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BASE COUNT 115 a 71 c 110 g 123 t
ORIGIN

Query Match 10.8%; Score 107.8; DB 8; Length 419;
Best Local Similarity 90.6%; Pred. No. 1.8e-13;
Matches 126; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 43 aggatatgatgattcattcgtctgtagtag-gcttcaactcttcgcatgtatcgtagca 101
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DB 281 AGGATATGATGATTATTATGGCTTAGACAGACCTTAACACCTCGCATGTATCGTGGA 340
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QY 102 tagcatcataaaatgtagcgtctgtagcatgttagtgtaggaagctatctta 161
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DB 341 TAGCATTTACATTAATAATGATTAAGCTTGCACCATGCGCTTAGAGGCGAAGGCTATCTTA 400
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QY 162 acttcattggaatgagtt 180
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DB 401 ATTTCATGGGAATGAGTT 419

Search completed: September 12, 2002, 07:30:44
Job time: 20832 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 08:21:51 : Search time 406.92 Seconds
(without alignments)
4223.512 Million cell updates/sec

Title: US-09-508-377-10_COPY_9500_10500

Perfect score: 1001
Sequence: 1 tccgacatgaacacagcatga.....ctggagcaatagctttttg 1001

Scoring table: IDENTITY_NUC
Gapop.10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 13: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1001	100.0	11473	20	AA34650
2	978	97.7	11475	22	AAH78338
3	223.2	22.3	23449	21	AA235393
4	136.4	13.6	2426	22	AAH78337
5	133.4	13.3	979	21	AA299942
6	130.2	13.0	977	21	AA299947
7	130.2	13.0	984	21	AA299946
8	118.8	11.9	3015	19	AAV05639
9	114.2	11.4	1085	21	AA299962

10	110.8	11.1	2087	18	AA269737	Corn starch branch
11	110.8	11.1	2165	18	AA269736	Corn starch branch
12	110.8	11.1	2640	19	AAV70961	DNA encoding maize
13	110.8	11.1	2665	18	AA269729	Pleasant 240. ins
14	110.8	11.1	2725	19	AA29737	Zea mays starch br
15	106	10.6	2919	15	AAQ73750	Rice starch branch
16	102.8	10.3	2307	21	AA299938	DNA encoding part
17	98	9.8	2968	22	AAH78342	Nucleotide sequenc
18	96.2	9.6	1087	21	AA299940	Nucleotide sequenc
19	95.2	9.5	1036	21	AA299939	Nucleotide sequenc
20	95.2	9.5	2913	19	AAV38719	Full length cassav
21	94.8	9.5	1069	19	AAV38721	Full length cassav
22	93.6	9.4	1919	19	AAV38722	CDNA encoding star
23	93.6	9.4	3003	17	AA242634	CDNA encoding star
24	93.6	9.4	3090	19	AAV38720	Class A starch bra
25	93	9.3	1120	21	AA299941	Full length cassav
26	92.8	9.3	2529	17	AA242637	Nucleotide sequenc
27	92.6	9.3	3074	18	AA269587	Class A starch bra
28	92	9.2	2531	17	AA217267	Potato starch bran
29	92	9.2	3033	17	AA242630	Class A starch bra
30	90.4	9.0	2576	17	AA242636	Class A starch bra
31	90.4	9.0	2578	17	AA242631	Class A starch bra
32	90.4	9.0	2975	17	AA242635	Class A starch bra
33	90.4	9.0	3231	17	AA242632	Class A starch bra
34	80.8	8.1	2715	21	AA245939	Arabidopsis thalia
35	79.2	7.9	1452	21	AA236957	Arabidopsis thalia
36	67.4	6.7	2899	22	AA202926	Human shear stress
37	67.4	6.7	3075	24	AA294880	Human DNA sequence
38	65.6	6.6	359	21	AA267263	Eucalyptus grandis
39	63.6	6.4	408	21	AA267266	Pinus radiata bran
40	60.8	6.1	2687	20	AA234646	WSBE I-D4 CDNA seq
41	60.8	6.1	4563	22	AA230910	Wheat starch bran
42	60.4	6.0	3128	16	AA200774	Potato starch bran
43	59.2	5.9	2487	18	AA269747	Corn starch branch
44	59.2	5.9	2565	18	AA269752	Corn starch branch
45	59.2	5.9	2713	19	AAV70962	DNA encoding maize

ALIGNMENTS

RESULT 1	AA34650	AA34650 standard; DNA: 11473 BP.
ID	AA34650	
AC	AA34650;	
XX		
DT	05-JUL-1999	(first entry)
XX		
DE	Starch branching enzyme II (SBE II) gene sequence.	
XX		
KW	Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSG;	
KW	starch branching enzyme; starch soluble synthase; debranching enzyme;	
KW	endosperm; wheat; barley; granule-bound synthase; glutennin; starch;	
KW	grain softness protein I; bacterial isoamylase; glycogen synthase;	
KW	WSBE I-D4 gene; ss.	
XX		
OS	Triticum tauschii.	
XX		
PN	W09914314-A1.	
XX		
PD	25-MAR-1999.	
XX		
PF	11-SEP-1998;	98WO-A000743.
XX		
PR	20-MAR-1998;	98AU-0002509.
PR	12-SEP-1997;	97AU-0009108.
XX		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
PA	(GOOD-) GOODMAN FIELDER LTD.	
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	
PA	(AUSU) UNIV AUSTRALIAN NAT.	
XX		


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Db 17932 gtttagagagagggcgtacatcttaattcatggaagatgttggacatcctgtgaga 17991
QY 198 ctttaacaattatgcatcttcgcatgattggtattactgta-----ttgaac 248
Db 17992 ttttaactactgttcatcttaactcctcgttgagctcttcttagaagactcctac 18051
QY 249 catgcttctcttcatcatgtaatgtaataatgtaataatgtaataatgtaataatg 308
Db 18052 aattactctgcaattatctcttctgttagtaataatgtaataatgtaataatg 18111
QY 309 ctctctatctatctgcaagaataatgtaataatgtaataatgtaataatgtaataat 368
Db 18112 ctctctatctatctgcaagaataatgtaataatgtaataatgtaataatgtaata 18171
QY 369 gcaaatcttccctggaataataatgtaataatgtaataatgtaataatgtaataat 428
Db 18172 gt-aagttatctccaggaataataataagtaataataagtaataataagtaata 18230
QY 429 gtaagtttagctgtgctatctacatccctcaactagatcttattgcca----- 478
Db 18231 gtaactctcttctgtgcaagaatgtaataatgtaataatgtaataatgtaata 18290
QY 479 -----ttattcttctgtaataatgtaataatgtaataatgtaataatgtaata 507
Db 18291 tgccttaacgaagagtgccatataatagttccctcttcttattcatattagatgt 18350
QY 508 tttaggaagatcaacatgctgttctgt-aggttgtgagcgttaataatagttgtgtg 565
Db 18351 agaagtaaaataatctacatcctctgttaaaagtttcttataatagttgtgtgtg 18410
QY 566 agagtgttgcattataaataatcatgattttt-----gcaaggagatcaaat 618
Db 18411 tcaataatctgcattatctcggaattgttatttttattcatctgcaagggtgagta 18470
QY 619 tcttagatctggtgcatcaagaatgtaataatgtaataatgtaataatgtaataat 678
Db 18471 tcttagatctggtgcatcaagaatgtaataatgtaataatgtaataatgtaata 18530
QY 679 tgggggagt-----tcaactgtgttcttctgtgcatataaagttacagttt 725
Db 18531 tgaagtaatgtcttcttcttcttcttcttcttcttcttcttcttcttcttctt 18590
QY 726 aacgtcagctctctcaagtgtaaaaaagtgtagaataatcctg-----taatg 777
Db 18591 attgtgtgcatcttcttcttcttcttcttcttcttcttcttcttcttcttctt 18650
QY 778 agatgaaacgtgcaaaagcgagctggaattgct-----ttcaocaaaactatttc 832
Db 18651 agcttttaagcaaatgaggtttcatatgaattcttctcatgtgcatcaacaact 18710
QY 833 ttaagtgtgtgtattgta----- 853
Db 18711 gtaatttcatgcatcttaaaagtaactctgagacagacgcaataatgtaacgaa 18770
QY 854 catataccagcagcgaacatgtaactgcaagttatgacatctgagacagcgaata 913
Db 18771 ttcttgatgaataattctgtgtaataatgcaagttatgacatctgacacagta 18830
QY 914 cggaaacatgaggaataatgtaataatgtaataatgtaataatgtaataatgtaata 973
Db 18831 cggaaacatgaggaataatgtaataatgtaataatgtaataatgtaataatgtaata 18890
QY 974 aacttcactgagcaatgctttttg 1001
Db 18891 aacttcactgagcaatgctttttg 18918

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RESULT 4
AAH78337
ID AAH78337 standard; cDNA; 2726 BP.
XX
AC AAH78337;
XX

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DT 26-NOV-2001 (first entry)
DE
XX Nucleotide sequence of wheat starch branching enzyme 9 (BEIIa).
XX
XX wheat; starch branching enzyme; BEIIa; BEIIb; SBE; transgenic plant;
KW starch biosynthetic pathway; amylopectin; amylose; ss.
XX
XX Triticum sp.
XX
XX WO200162934-A1.
XX
XX 30-AUG-2001.
XX
XX 21-FEB-2001; 2001MO-AU00175.
XX
XX 21-FEB-2000; 2000AU-0005742.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX (GOOD-) GOODMAN FIELDER LTD.
XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
XX Morell M, Rahman S;
XX
XX WPI; 2001-570635/64.
XX
XX Nucleic acids encoding wheat starch branching enzyme IIb, useful for
PT altering the amylose and amylopectin content of cereal plants, e.g.
PT wheat and barley -
XX
XX Example 1; Fig 1; 103pp; English.
XX
XX The present sequence encodes wheat starch branching enzyme 9,
XX designated BEIIa. The specification describes BEIIb. BEIIb is a
XX type II starch branching enzyme (SBE). The BEIIb nucleic acids may
XX be used to genetically transform cereal plants such as wheat or
XX barley and for altering their nutritional content by modulating
XX the starch biosynthetic pathway to vary levels of amylopectin and/or
XX amylose produced in the plant.
XX
XX Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 other;
XX

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Query Match 13.6%; Score 136.4; DB 22; Length 2726;
Best Local Similarity 98.7%; Pred. No. 1.9e-25;
Matches 148; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 43 aggatatgatgatcttcacgtctctgataag-cttcaactcttcgcatgacgtgga 101
Db 1787 aggatatgatgatcttcacgtctctgataagcttcacactcttcgcatgacgtgga 1846

QY 102 tagcatataataatgataagcttgcacatgggttagtgtgaagctatctta 161
Db 1847 tagcatataataatgataagcttgcacatgggttagtgtgaagctatctta 1906

QY 162 acttcattggaatgagttggacatcgt 191
Db 1907 acttcattggaatgagttggacatcgt 1936

RESULT 5
AAZ99942
ID AAZ99942 standard; DNA; 979 BP.
XX
XX AAZ99942;
XX
XX 25-JUL-2000 (first entry)
XX
XX Nucleotide sequence of starch branching enzyme II clone B1.
XX
XX wheat; starch branching enzyme II; SBEII; SBEII-2; starch; SBEII-1;
KW gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX
XX Triticum aestivum.
XX

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```
XX XX WO200015810-A1.
XX XX 23-MAR-2000.
XX XX
XX XX 09-SEP-1999; 99WO-GB03011.
XX XX 10-SEP-1998; 98EP-0307337.
XX XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.
XX XX Goldsbrough A, Colliver S;
XX XX WPI; 2000-271446/23.
XX XX
XX XX DNA encoding wheat starch branching enzyme II isoforms, useful in
XX XX altering the characteristics of a plant, especially elevated starch
XX XX gelatinization onset and/or peak temperature -
XX XX
XX XX Claim 5; Page 124; 197pp; English.
XX XX
XX XX The present sequence represents a clone of wheat starch branching
XX XX enzyme II (SBEII), which is part of a novel subclass of known SBEII
XX XX genes, designated SBEII-2, subclass B (SBEII-2B). The specification also
XX XX describes subclasses SBEII-1 genes, which are thought to have similar
XX XX functional properties to the maize SBEII gene. Starch branching enzymes
XX XX catalyse the formation of the alpha-1,6 linkages, creating branch points
XX XX in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage
XX XX followed by reattachment of the released alpha-1,4-glucan chain to the
XX XX same or another glucosyl chain. SBEII polypeptides can be used to alter
XX XX the characteristics of a plant, in particular to alter starch so that
XX XX it has an elevated gelatinisation onset and/or peak temperature. Starch
XX XX obtained from transgenic plants is useful in the preparation or
XX XX processing a foodstuff, particularly bakery products.
XX XX
XX XX Sequence 979 BP; 271 A; 203 C; 247 G; 257 T; 1 other;
XX XX
XX XX Query Match 13.3%; Score 133.4; DB 21; Length 979;
XX XX Best Local Similarity 98.6%; Pred. No. 8.4e-25;
XX XX Matches 145; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX XX
XX XX QY 46 atatgatgatcttcagctctgtgataag-cttcaactcttcgcatgatcgtgcatag 104
XX XX |||||||
XX XX Db 1 atatgatgatcttcagctctgtgataag-cttcaactcttcgcatgatcgtgcatag 60
XX XX
XX XX QY 105 cattacataaaatgatcagctctgtcaccatgggttagtgggtgaagcctacttaact 164
XX XX |||||||
XX XX Db 61 cattacataaaatgatcagctctgtcaccatgggttagtgggtgaagcctacttaact 120
XX XX
XX XX QY 165 tcatgggaaatgatgttgggcattcctg 191
XX XX |||||||
XX XX Db 121 tcatgggaaatgatgttgggcattcctg 147
XX XX
XX XX RESULT 6
XX XX AAZ99947
XX XX ID AAZ99947 standard; DNA; 977 BP.
XX XX
XX XX AC AAZ99947;
XX XX
XX XX 25-JUL-2000 (first entry)
XX XX
XX XX Nucleotide sequence of starch branching enzyme II clone B11.
XX XX
XX XX Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;
XX XX gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX XX
XX XX Triticum aestivum.
XX XX
XX XX Key Location/Qualifiers
XX XX FT CDS 3..641
XX XX FT /*tag- a
XX XX FT
```

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FT XX /product- "starch branching enzyme II"
XX XX
XX XX WO200015810-A1.
XX XX 23-MAR-2000.
XX XX
XX XX 09-SEP-1999; 99WO-GB03011.
XX XX 10-SEP-1998; 98EP-0307337.
XX XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.
XX XX Goldsbrough A, Colliver S;
XX XX WPI; 2000-271446/23.
XX XX P-PSDB; AAY84411.
XX XX
XX XX DNA encoding wheat starch branching enzyme II isoforms, useful in
XX XX altering the characteristics of a plant, especially elevated starch
XX XX gelatinization onset and/or peak temperature -
XX XX
XX XX Disclosure; Page 168-169; 197pp; English.
XX XX
XX XX The present sequence represents a clone of wheat starch branching
XX XX enzyme II (SBEII), which is part of a novel subclass of known SBEII
XX XX genes, designated SBEII-1. The specification also describes subclass
XX XX SBEII-2 sequences. The SBEII-1 genes are thought to have similar
XX XX functional properties to the maize SBEII gene. Starch branching enzymes
XX XX catalyse the formation of the alpha-1,6 linkages, creating branch points
XX XX in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage
XX XX followed by reattachment of the released alpha-1,4-glucan chain to the
XX XX same or another glucosyl chain. SBEII polypeptides can be used to alter
XX XX the characteristics of a plant, in particular to alter starch so that
XX XX it has an elevated gelatinisation onset and/or peak temperature. Starch
XX XX obtained from transgenic plants is useful in the preparation or
XX XX processing a foodstuff, particularly bakery products.
XX XX
XX XX Sequence 977 BP; 270 A; 200 C; 245 G; 262 T; 0 other;
XX XX
XX XX Query Match 13.0%; Score 130.2; DB 21; Length 977;
XX XX Best Local Similarity 97.3%; Pred. No. 5.7e-24;
XX XX Matches 143; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
XX XX
XX XX QY 46 atatgatgatcttcagctctgtgataag-gcttcaactcttcgcatgatcgtgcatag 104
XX XX |||||||
XX XX Db 1 atatgatgatcttcagctctgtgataag-gcttcaactcttcgcatgatcgtgcatag 60
XX XX
XX XX QY 105 cattacataaaatgatcagctctgtcaccatgggttagtgggtgaagcctacttaact 164
XX XX |||||||
XX XX Db 61 cattacataaaatgatcagctctgtcaccatgggttagtgggtgaagcctacttaact 120
XX XX
XX XX QY 165 tcatgggaaatgatgttgggcattcctg 191
XX XX |||||||
XX XX Db 121 tcatgggaaatgatgttgggcattcctg 147
XX XX
XX XX RESULT 7
XX XX AAZ99946
XX XX ID AAZ99946 standard; DNA; 984 BP.
XX XX
XX XX AC AAZ99946;
XX XX
XX XX 25-JUL-2000 (first entry)
XX XX
XX XX Nucleotide sequence of starch branching enzyme II clone A2.
XX XX
XX XX Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;
XX XX gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX XX
XX XX Triticum aestivum.
XX XX
XX XX WO200015810-A1.
XX XX PN
```


PD	23-MAR-2000.
XX	
XX	09-SEP-1999; 99WO-GB03011.
PF	
XX	10-SEP-1998; 98EP-0307337.
PR	
XX	
PA	(PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.
XX	
XX	Goldsbrough A, Collier S;
PI	
DR	WPI; 2000-271446/23.
XX	
XX	
PT	DNA encoding wheat starch branching enzyme II isoforms, useful in
PT	altering the characteristics of a plant, especially elevated starch
PT	gelatinization onset and/or peak temperature -
XX	
PS	Disclosure: Page 168; 197pp; English.
XX	
CC	The present sequence represents a clone of wheat starch branching
CC	enzyme II (SBEII), which is part of a novel subclass of known SBEII
CC	genes, designated SBEII-1. The specification also describes subclass
CC	SBEII-2 sequences. The SBEII-1 genes are thought to have similar
CC	functional properties to the maize SBEII gene. Starch branching enzymes
CC	catalyse the formation of the alpha-1,6 linkages, creating branch points
CC	in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage
CC	followed by reattachment of the released alpha-1,4-glucan chain to the
CC	same or another glucosyl chain. SBEII polypeptides can be used to alter
CC	the characteristics of a plant, in particular to alter starch so that
CC	it has an elevated gelatinisation onset and/or peak temperature. Starch
CC	obtained from transgenic plants is useful in the preparation or
CC	processing a foodstuff, particularly bakery products.
XX	
XX	Sequence 984 BP; 268 A; 212 C; 250 G; 254 T; 0 other;

Query Match	13.0%	Score 130.2	DB 21	Length 984
Best Local Similarity	97.3%	Pred. No. 5,7e-24		
Matches 143	Conservative 0	Mismatches 3	Indels 1	Gaps 1
Oy	46	atatgatcatcttagctcgtcgtgtag-gctcaactcttcgattgactgtgtgcatag	104	
Db	1	atacgtatgatcttcacatgctcctgataagaccttcaactcttcgattgactgtgcatag	60	
Oy	105	cattacataaatagtatcaggctctgcacacatggtttagtgtgtgaaggctacttaact	164	
Db	61	cattacataaatagtatcaggctctgcacacatggtttagtgtgtgaaggctacttaact	120	
Oy	165	tcatgtggaaatgagtttgggcatcctg	191	
Db	121	tcatgtggaaatgagtttgggcatcctg	147	

RESULT 8

AAV05639	AAV05639 standard; cDNA to mRNA; 3015 BP.
AC	AAV05639;
XX	
DT	01-MAY-1998 (first entry)
XX	
DE	Rice type IV starch branching enzyme cDNA.
XX	
KW	Rice; type IV starch branching enzyme; amylopectin synthesis; ds.
XX	
OS	Oryza sativa.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	129..2654
FT	/*tag=a
FT	sig_peptide
FT	129..287
FT	/*tag=b
FT	mat_peptide
FT	288..2651

FT	/*tag=	C
FT	/product=	type_IV_starch_branching_enzyme
XX		
PN	JP10004970-A.	
XX		
PD	13-JAN-1998.	
XX		
PF	24-JUN-1996;	96JP-0162983.
XX		
PR	24-JUN-1996;	96JP-0162983.
XX		
PA	(MITS-) MITSUI GROSAI SHOKUBUNSU BIO KENKYUSHO.	
PA	(MITK) MITSUI TOATSU CHEN INC.	
XX		
DR	WPI; 1998-133625/13.	
DR	P-PSDB; AAW41763.	
XX		
PT	Rice starch branching enzyme gene - synthesises amylopectin to yield	
XX	high quality starch	
PS	Claim 4; Pages 5-8; 13pp; Japanese.	
XX		
CC	The present sequence encodes the rice type IV starch branching	
CC	enzyme, which has the ability to synthesise amylopectin. The	
CC	quality of starch is improved by the use of the protein.	
XX		
SQ	Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;	

Query Match	11.98;	Score 118.8;	DB 19;	Length 3015;
Best Local Similarity	91.3%;	Pred. No. 7.3e-21;		
Matches 137;	Conservative	0;	Mismatches 12;	Indels 1;
				Gaps 1.
Qy	43	aggataatgatgattcattcagtcctctgagatag-gcttcaactcttcgcatgatacgtgca	101	
Db	2008	aggataatgatgatttattgattctcagacagacaccttcaacacacctcgcatgatacgtgga	2067	
Qy	102	tatgattacataataatgatcagagcttctccacatgggttaagtgtgaagctactcta	161	
Db	2068	tatgattacataataatgatgattagctctgtccacatgggtcttagagagcgaaagctactcta	2127	
Qy	162	acttcatgggaaatgaatttgggcactccty	191	
Db	2128	attcattgggaaatgaatttgggcactccty	2157	
RESULT 9				
AAZ99962				
ID	AAZ99962	standard; DNA; 1085	BP.	
XX				
XX	AAZ99962;			
XX				
DT	25-JUL-2000	(first entry)		
XX				
DE	Consensus sequence of starch branching enzyme II.			
XX				
KW	Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;			
KN	gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.			
XX				
OS	Triticum aestivum.			
XX				
FN	WO200015810-A1.			
XX				
PD	23-MAR-2000.			
XX				
PF	09-SEP-1999;	99WO-GB03011.		
XX				
PR	10-SEP-1998;	98EP-0307337.		
XX				
PA	(PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.			
XX				
PI	Goldsbrough A.	Colliver S;		
XX				

DR WPI; 2000-271446/23.

XX DNA encoding wheat starch branching enzyme II isoforms, useful in
 PT altering the characteristics of a plant, especially elevated starch
 PT gelatinization onset and/or peak temperature -
 XX
 XX Disclosure; Page 187; 197pp; English.

PS The present sequence represents the consensus sequence of wheat starch
 CC branching enzyme II (SBEII). The specification describes novel subclasses
 CC of SBEII, designated SBEII-1 and SBEII-2. The SBEII-1 genes are thought
 CC to have similar functional properties to the maize SBEIIb gene. Starch
 CC branching enzymes catalyze the formation of the alpha-1,6 linkages,
 CC creating branch points in the growing starch molecule, via hydrolysis of
 CC an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-
 CC glucan chain to the same or another glucosyl chain. SBEII polypeptides
 CC can be used to alter the characteristics of a plant, in particular to
 CC alter starch so that it has an elevated gelatinization onset and/or peak
 CC temperature. Starch obtained from transgenic plants is useful in the
 CC preparation or processing a foodstuff, particularly bakery products.

CC
 XX Sequence 1085 BP; 268 A; 185 C; 284 G; 348 T; 0 other:

Query Match 11.4%; Score 114.2; DB 21; Length 1085;
 Best Local Similarity 90.5%; Pred. No. 8.2e-20;
 Matches 133; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

OY 46 atatgatatattcatgctctgtagag-gcttcaactcttcgcatgtgtagatg 104
 Db 1 atatgatatattcatgctctgtagag-gcttcaactcttcgcatgtgtagatg 60
 OY 105 cattacataaattgatcagagctgtccacatggttagtggtagaaggcatcttaact 164
 Db 61 cattgacataaattgatgtagctgtccacatggttagtggtagaaggcatcttaact 120
 OY 165 tcatgggaatgagttgggcatctg 191
 Db 121 tcatgggaatgagttgggcatctg 147

RESULT 10
 AAT69737
 ID AAT69737 standard; DNA; 2087 BP.
 XX
 AC AAT69737;
 XX
 DT 10-SEP-1997 (first entry)
 XX
 DE Corn starch branching enzyme IIB gene fragment in pBE96.
 XX
 KW Starch branching enzyme IIB; SBEIIB; corn; maize; antisense;
 KW amylopectin; transgenic plant; pBE96; ss.
 XX
 OS Zea mays.
 XX
 PN WO9722703-A2.
 XX
 PD 26-JUN-1997.
 XX
 PF 12-DEC-1996; 96WO-US19678.
 XX
 PR 20-DEC-1995; 95US-0009113.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Broglie KE, Hubbard NL, Klein TW;
 XX
 DR WPI; 1997-341694/31.
 XX
 PT Transgenic corn in which grain derived starch fine structure is
 PT controlled - specifically branch chain distribution of amylopectin,
 PT useful in preparation of thickened foodstuff

XX Example 4; Page 56-57; 92pp; English.

PS A cDNA insert (AAT69737) in plasmid pBE96 comprises a 2.09 kb
 XX fragment of corn starch branching enzyme IIB (SBEIIB) cDNA (see
 CC also AAT69729), starting at the initiating ATG codon of the coding
 CC region and terminating 312 bp 5' of the translation termination
 CC codon. It was obt. by site-specific mutagenesis of the SBEIIB
 CC gene in plasmid pBE240 to generate an NcoI site at the ATG start
 CC site, and EcoRI digestion of the mutagenised plasmid. The 2.09 kb
 CC fragment was inserted, in sense orientation, between the zein
 CC promoter and 3' regions in vector pM103 to produce pBE96.
 CC Co-suppression and antisense techniques can be used to inhibit
 CC SBEIIB in transgenic plants and thereby alter starch properties.

CC
 XX Sequence 2087 BP; 565 A; 396 C; 553 G; 573 T; 0 other:

Query Match 11.1%; Score 110.8; DB 18; Length 2087;
 Best Local Similarity 88.0%; Pred. No. 7.6e-19;
 Matches 132; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

OY 43 aggatatgatatttcatgctctgtagag-gcttcaactcttcgcatgtgtagca 101
 Db 1757 aggatatgatatttcatgctctgtagag-gcttcaactcttcgcatgtgtagca 1816
 OY 102 tagcatataaattgatcagagctgtccacatggttagtggtagaaggcatctta 161
 Db 1817 tagcatataaattgatgtagtagaactatcacatggttagtggtagaaggcatctta 1876
 OY 162 acttcattggaatgagttgggcatctg 191
 Db 1877 attcattggaatgagttgggcatctg 1906

RESULT 11
 AAT69736/C
 ID AAT69736 standard; DNA; 2165 BP.
 XX
 AC AAT69736;
 XX
 DT 10-SEP-1997 (first entry)
 XX
 DE Corn starch branching enzyme IIB gene fragment in pBE45.
 XX
 KW Starch branching enzyme IIB; SBEIIB; corn; maize; antisense;
 KW amylopectin; transgenic plant; pBE45; ss.
 XX
 OS Zea mays.
 XX
 PN WO9722703-A2.
 XX
 PD 26-JUN-1997.
 XX
 PF 12-DEC-1996; 96WO-US19678.
 XX
 PR 20-DEC-1995; 95US-0009113.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Broglie KE, Hubbard NL, Klein TW;
 XX
 DR WPI; 1997-341694/31.
 XX
 PT Transgenic corn in which grain derived starch fine structure is
 PT controlled - specifically branch chain distribution of amylopectin,
 PT useful in preparation of thickened foodstuff

Example 3; Page 55-56; 92pp; English.

CC A 2.16 kb cDNA insert (AAT69736) in plasmid pBE45 comprises the
 CC entire 5' untranslated region as well as 2.08 kb of the coding
 CC region of corn starch branching enzyme IIB (SBEIIB) cDNA (see

XX Sequence 2665 BP; 700 A; 525 C; 705 G; 735 T; 0 other;
SQ

Query Match 11.1%; Score 110.8; DB 18; Length 2665;
Best Local Similarity 88.0%; Pred. No. 8.2e-19;
Matches 132; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 43 aggatatgatgatcctcgtgatag-gctcaactcttgcatgacgtgcca 101
|||||
DB 1835 aggatatgatgatcctcgtgatag-gctcaactcttgcatgacgtgcca 1894
QY 102 tagcattacataaagatcagcctgtgcacatgggttaggtggaagctatctta 161
|||||
DB 1895 tagcattacataaagatcagcctgtgcacatgggttaggtggaagctatctta 1954
QY 162 acttcattgggaatgagtttggtgacatccgt 191
|
DB 1955 attcatgggaatgagtttggtgacatccgt 1984

RESULT 14

AAV29757
ID AAV29757 standard; DNA; 2725 BP.

AC AAV29757;

DT 11-SEP-1998 (first entry)

DE Zea mays starch branching enzyme II gene.

KW SER; starch-encapsulating region; fusion vector;

KM starch branching enzyme II; ss.

OS Zea mays.

EH Key Location/Qualifiers

FT CDS 91..2490

FT /tag= a

FT /product= starch branching enzyme II

FT sig_peptide 91..264

FT /tag= b

FT mat_peptide 265..2487

FT /tag= c

PN MO9814601-A1.

PD 09-APR-1998.

PF 30-SEP-1997; 97WO-US17555.

PR 30-SEP-1996; 96US-0026655.

PA (EXSE-) EXSEED GENETICS LLC.

PI Guan H, Keeling P;

DR WPI: 1998-240100/21.

DR P-PSDB; AAW56489.

XX Hybrid polypeptide comprising starch-encapsulating region and
PT protein - useful for, e.g. producing protein(s) resistant to
PT degradation by stomach acids

PS Example 2; Page 44; 156pp; English.

CC The sequence is that of the starch branching enzyme II gene.

CC It can be used in the production of a hybrid polypeptide
CC comprising a starch-encapsulating region (SER) fused

CC to a payload protein. The hybrid polypeptide can be used to make
CC modified starches comprising the payload protein, selected from,

CC e.g. hormones, growth factors, antibodies, enzymes, dyes,
CC immunoglobulins, etc. The modified starch can also be used

CC to provide grain feeds enriched in amino acids. By encapsulating
CC the payload protein in starch, it is more resistant to
CC degradation by stomach acids.

XX Sequence 2725 BP; 727 A; 534 C; 715 G; 749 T; 0 other;
SQ

Query Match 11.1%; Score 110.8; DB 19; Length 2725;
Best Local Similarity 88.0%; Pred. No. 8.3e-19;
Matches 132; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 43 aggatatgatgatcctcgtgatag-gctcaactcttgcatgacgtgcca 101
|||||
DB 1847 aggatatgatgatcctcgtgatag-gctcaactcttgcatgacgtgcca 1906
QY 102 tagcattacataaagatcagcctgtgcacatgggttaggtggaagctatctta 161
|||||
DB 1907 tagcattacataaagatcagcctgtgcacatgggttaggtggaagctatctta 1966
QY 162 acttcattgggaatgagtttggtgacatccgt 191
|
DB 1967 attcatgggaatgagtttggtgacatccgt 1996

RESULT 15

AAO73750
ID AAO73750 standard; cDNA to mRNA; 2919 BP.

AC AAO73750;

DT 05-JUL-1995 (first entry)

DE Rice starch branching enzyme.

KW Starch branching enzyme; rice; starch content; ds.

OS Oryza sativa.

EH Key Location/Qualifiers

FT 5'UTR 1..127

FT /tag= a

FT transit_peptide 128..322

FT /tag= b

FT mat_peptide 323..2606

FT /tag= c

FT /product= branching_enzyme

FT 3'UTR 2603..2919

FT /tag= d

PN JP06261767-A.

PD 20-SEP-1994.

PF 22-OCT-1993; 93UP-0265171.

PR 29-OCT-1992; 92UP-0291719.

PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

DR WPI: 1994-337418/42.

DR P-PSDB; AAR60811.

XX New gene of branching enzyme of rice starch - useful for
PT increasing starch yield of rice grains
PT
PS Claim 1; Page 9-12; 13pp; Japanese.

CC The rice starch branching enzyme is encoded by the cDNA sequence

CC AAO73750. The starch content of rice grains can be increased by
CC increasing the expression of branching enzyme in rice plants.

XX Sequence 2919 BP; 755 A; 590 C; 800 G; 774 T; 0 other;
SQ

Query Match 10.6%; Score 106; DB 15; Length 2919;
Best Local Similarity 86.0%; Pred. No. 1.5e-17;
Matches 129; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 43 aggatatgtatgtatcattcagctcttgagatag-gcttcaactcttcgcatltgctgtgca 101
|||||
Db 1962 aggatatgtatgtattttatgtctcttgacagacgcgcaacacctagcatgtatcgttgaa 2021
|||||

QY 102 tagcattacataaataatgatcaggcttgtcacatgggtttaggtgtgtaaggctatctta 161
|||||
Db 2022 tagcatgtcataaataatgatcaggcttgtcacatgggtttaggtgtgtaaggctatctta 2081
|||||

QY 162 acttcatgggaaatgagtttgggcatcctg 191
|||||
Db 2082 acttcatgggaaatgagtttgggcatcctg 2111
|||||

Search completed: September 12, 2002, 08:22:35
Job time: 12312 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 08:12:56 ; Search time 92.79 Seconds
(without alignments)
2649.845 Million cell updates/sec

Title: US-09-508-377-10_COPY_9500_10500

Perfect score: 1001

Sequence: 1 tcgcagcatagacagcatga.....ctggagcatagctttttt 1001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :
1: Issued_Patents_NA:*
2: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
3: /cgn2_6/ptodata/1/lna/5B_COMB.seq:*
4: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
5: /cgn2_6/ptodata/1/lna/5B_COMB.seq:*
6: /cgn2_6/ptodata/1/lna/PTOTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110.8	11.1	2725	3	US-08-941-445A-14
2	94.2	9.4	3074	4	US-09-087-277-1
3	92.6	9.3	1393	4	US-09-087-277-3
4	60.4	6.0	3128	3	US-08-716-449-1
5	59.2	5.9	2763	3	US-08-941-445A-16
6	46.2	4.6	2909	4	US-08-104-158-1
7	40.6	4.1	2132	3	US-08-844-188-39
8	36.6	3.7	11478	3	US-08-332-463-14
9	36.6	3.7	11478	4	US-08-981-803-29
10	36.6	3.7	11478	4	US-08-983-440-29
11	36.4	3.6	2088	4	US-09-351-414-3
12	36	3.6	3607	4	US-08-647-351B-1
13	35.8	3.6	5801	4	US-09-177-249-5
14	35.2	3.5	1945	2	US-08-525-742-5
15	34.2	3.4	3418	4	US-09-193-562D-29
16	34	3.4	3607	1	US-08-647-351B-1
17	33.8	3.4	782	1	US-08-261-825-1
18	33.8	3.4	782	2	US-08-719-124-1
19	33.8	3.4	782	5	PCT-US95-07748-1
20	33.8	3.4	782	5	PCT-US95-07748A-1
21	33.8	3.4	1850	2	US-08-617-860B-32
22	33.8	3.4	4098	2	US-08-605-106-4
23	33.2	3.3	2368	3	US-08-714-918-2
24	33.2	3.3	2368	4	US-09-265-315-2
25	33.2	3.3	2368	4	US-09-265-315-2
26	33.2	3.3	2368	4	US-09-266-417-2
27	33.2	3.3	7218	1	US-08-232-463-14

C 28	32.33	3	3	3763	1	US-07-792-865D-1	Sequence 1, Appl
C 29	32.4	3	2	685	4	US-09-122-400B-10	Sequence 10, Appl
C 30	32.4	3	2	2395	3	US-08-985-335-6	Sequence 6, Appl
C 31	32.4	3	2	2395	4	US-09-410-372-6	Sequence 6, Appl
C 32	32.4	3	2	2510	4	US-08-894-324A-2	Sequence 2, Appl
C 33	32.2	3	2	665	2	US-08-883-795A-36	Sequence 36, Appl
C 34	32.2	3	2	848	4	US-08-905-223-27	Sequence 27, Appl
C 35	32.2	3	2	848	4	US-09-247-155-27	Sequence 27, Appl
C 36	32.2	3	2	15462	4	US-09-073-492-1	Sequence 1, Appl
C 37	32.2	3	2	16442	3	US-08-781-891-208	Sequence 208, Appl
C 38	31.8	3	2	845	4	US-09-227-357-120	Sequence 120, Appl
C 39	31.8	3	2	1447	4	US-09-227-357-17	Sequence 17, Appl
C 40	31.8	3	2	2558	1	US-08-477-776-1	Sequence 1, Appl
C 41	31.8	3	2	2558	2	US-08-993-210-1	Sequence 1, Appl
C 42	31.8	3	2	2558	5	PCT-US96-07354-1	Sequence 1, Appl
C 43	31.8	3	2	3771	1	US-07-876-280-5	Sequence 5, Appl
C 44	31.8	3	2	3771	1	US-08-049-783-1	Sequence 1, Appl
C 45	31.8	3	2	3771	1	US-08-158-232-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-941-445A-14
; Sequence 14, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026, 855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; TELEPHONE: (303) 499-8080
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 89-97
; TELEFAX: (303) 499-8080
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2725 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: mRNA
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..264
; FEATURE:
; NAME/KEY: mat_peptide

LOCATION: 265..2487
FEATURE:
NAME/KEY: CDS
LOCATION: 91..2490
US-08-941-445A-14

Query Match 11.1%; Score 110.8; DB 3; Length 2725;
Best Local Similarity 88.0%; Pred. No. 6.8e-22;
Matches 132; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 43 aggatgatgatattcattcagctctgtagtag-gcttcaactcttcgcatgtagcgca 101
|||||
Db 1847 AGGATGATGATGATTTCAAGCCCTCGATAGACCTTCACTTACCATGATGATGGA 1906
|||||
QY 102 tagcatataaataatgacagctgtcaccaatgggttagtggtgaagctatccta 161
|||||
Db 1907 TAGCATATACATAAGATGATTAGACTTATACACATGGGTTTAGAGAGAGGCTATCTTA 1966
|||||
QY 162 actcaatgggaatgaggttggtgcatcctg 191
|||||
Db 1967 ATTTCATGGAAATGAGTTTGGACATCTCG 1996
|||||

RESULT 2
US-09-087-277-1
Sequence 1, Application US/09087277B
Patent No. 6169226

GENERAL INFORMATION:

APPLICANT: EK, Bo

APPLICANT: KHOSNODI, Jamshid

APPLICANT: LARSSON, Clas-Tomas

APPLICANT: RASK, Lars

TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO

FILE REFERENCE: 003300-486

CURRENT APPLICATION NUMBER: US/09/087,277B

EARLIER FILING DATE: 1998-05-29

EARLIER APPLICATION NUMBER: PCT/SE96/01558

EARLIER FILING DATE: 1996-11-28

EARLIER APPLICATION NUMBER: SE 9504272-7

EARLIER FILING DATE: 1995-11-29

EARLIER APPLICATION NUMBER: SE 9601506-0

EARLIER FILING DATE: 1996-04-19

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 3074

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism:bell gene

OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum

FEATURE:

NAME/KEY: CDS

LOCATION: (189)..(2825)

FEATURE:

NAME/KEY: sig_peptide

LOCATION: (189)..(332)

FEATURE:

NAME/KEY: mat_peptide

LOCATION: (333)..(2825)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (92)..(2156)

OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are

OTHER INFORMATION: n wherein n = A, C, G or T.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (285)..(287)

OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val

OTHER INFORMATION: or Phe.

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys

FEATURE:
NAME/KEY: misc_feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: or Phe.

US-09-087-277-1
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.

Query Match 9.4%; Score 94.2; DB 4; Length 3074;
Best Local Similarity 78.1%; Pred. No. 3.5e-17;
Matches 125; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 33 cctcttgacagatatgatattcattcagctctgtagtag-gcttcaactcttcgcat 91
|||
Db 2112 cctgatggaagaagatatgatatttattgctctgtagtagccttcaacatcataata 2171
|||||
QY 92 gatctgtgcatatgacataaataatgacagctgtgtacatggtttagtggtgaa 151
|||||
Db 2172 gatcgttgagtagatgacacaaagatgtagctgtgtaactatgtagtagagagaa 2231
|||||
QY 152 ggcatacttaactcatggaatgagtttggtgcatcctg 191
|||
Db 2232 gggtaoctaattcattcatggaatgagtttggtgcatcctg 2271
|||||

RESULT 3
US-09-087-277-3
Sequence 3, Application US/09087277B
Patent No. 6169226

GENERAL INFORMATION:

APPLICANT: EK, Bo

APPLICANT: KHOSNODI, Jamshid

APPLICANT: LARSSON, Clas-Tomas

APPLICANT: RASK, Lars

TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO

FILE REFERENCE: 003300-486

CURRENT APPLICATION NUMBER: US/09/087,277B

EARLIER FILING DATE: 1998-05-29

EARLIER APPLICATION NUMBER: PCT/SE96/01558

EARLIER FILING DATE: 1996-11-28

EARLIER APPLICATION NUMBER: SE 9504272-7

EARLIER FILING DATE: 1995-11-29

EARLIER APPLICATION NUMBER: SE 9601506-0

EARLIER FILING DATE: 1996-04-19

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 1393

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism:bell gene fragment

OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum

FEATURE:

NAME/KEY: CDS

LOCATION: (2)..(1393)

OTHER INFORMATION: (potato)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (424)..(1150)

RESULT 5
US-08-941-445A-16
Sequence 16, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Haining
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-Sep-1997
CLASSIFICATION: 800


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; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/844.188
; APPLICATION NUMBER: US/08/844.188
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/633,993
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-703C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-844-188-39

```

```

Query Match      4.1%; Score 40.6; DB 3; Length 2132;
Best Local Similarity 51.4%; Pred. No. 0.041;
Matches 94; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 490 atgaatcataatgttcttgaagaagaatcaaatcttcttgaagcgtta 549
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2009 ATACGATTATCTTCAAAATTAATTAAGATTATCTTGGTTTGAATTAAT 1950
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 550 acataagatagtggtgagagtggtgacatcaataaatacatgatttttcagggaga 609
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1949 TCTAATTTCATATTTAAAAAATATATTTTAAATTTTAAAGTACTTTAAGATA 1890
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 610 tgcagattcttagatalcgtlgtatgcagagttcgatcaggaatgcagcatcttga 669
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1889 TTTGTTATTTCTTCTACCTTCATATGATGATTTGTAAGAATTAAGCTTGTGA 1830
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 670 gga 672
    ||
DB 1829 TGA 1827

```

```

RESULT 8
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFFLINGER, F.
; APPLICANT: PARKER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/232.463
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

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Query Match      3.7%; Score 36.6; DB 1; Length 7218;
Best Local Similarity 5.4%; Pred. No. 0.95;
Matches 18; Conservative 174; Mismatches 143; Indels 0; Gaps 0;

QY 154 ctatcttaactcatcaggaatagttggcgtcgtcagctcttaccacattatg 213
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1034 CGAGCTTGCGCTGACGCTGAGGAGGACTTGCGATTTTTTTTTTTTTTTTTT 1093
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 214 catctcgaatgatgttgaattgaattgaaccatgcttcttccatgtatgt 273
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1094 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1153
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 274 ataatgatactgttgcctccaaggaagaattactcttattctctgcgaatgat 333
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1154 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1213
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 334 agatttccaagagcccaacaactctccaacgcgcaagttccctcggaataaca 393
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1214 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1273
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 394 atagtaataaalgccgcgtagattgatactgttaagtttagctgtcattatc 453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1274 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1333
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 454 tccctcaactagatccttattggccattattctt 488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1334 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 9
US-08-981-803-29
; Sequence 29, Application US/08981803
; Patent No. 6147279
; GENERAL INFORMATION:
; APPLICANT: FOULSEN, PETER
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2004
; CURRENT APPLICATION NUMBER: US/08/981,803
; CURRENT FILING DATE: 1997-04-17
; EARLIER APPLICATION NUMBER: PCT/EP96/03052
; EARLIER FILING DATE: 1996-07-12

```

```

1  EARLIER APPLICATION NUMBER: 95114435.8
2  EARLIER FILING DATE: 1995-07-14
3  NUMBER OF SEQ. ID NOS: 33
4  SOFTWARE: PatentIn Ver. 2.0
5  SEQ ID NO 29
6  LENGTH: 11478
7  TYPE: DNA
8  ORGANISM: Solanum tuberosum
9  OS-08-981-803-29

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Query Match	3.7%	Score	36.6	DB	3	Length	11478
Best Local Similarity	65.1%	Pred. No.	1.2				
Matches	54	Conservative	0	Mismatches	29	Indels	0
						Gaps	0

Qy 107 ttacataaaatgatcaggccttgcaccatggttttcgttgtaagcctaacttca 166
| | | | | | | | | | | | | | | | | |
Db 6667 taaccacagatgcccatctttcacaatgcttggagagaggytlacctcaatttc 6726

Qy	167	atgggaatgagtttggcatcc	189
Db	6727	atggtaacgagtgatgtcttac	6749

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RESULT 10
US-08-983-440-29
Sequence 29, Application US/08983440
Patent No. 6232122
GENERAL INFORMATION:
APPLICANT: POULSEN, Peter
TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 674509-2003
CURRENT APPLICATION NUMBER: US/08/983,440
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER FILING DATE: 1995-07-14
EARLIER APPLICATION NUMBER: PCT/EP96/03053
EARLIER FILING DATE: 1996-07-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 11478
TYPE: DNA
ORGANISM: Solanum tuberosum
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: B stands for G or C or T/U
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: R stands for G or A
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: K stands for G or T/U
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: W stands for A or T/U
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: M stands for A or C
US-08-983-440-29

```

Query Match	3.7%	Score	36.6	DB	4	Length	11478
Best Local Similarity	65.1%	Pred. No.	1.2				
Matches	54	Conservative	0	Mismatches	29	Indels	0
						Gaps	0

QY 107 ttacataaatgatcagctgtgcaccatgggttttggtggtgaaggctatcctaacttc 166
||| ||||||| ||||||| ||| ||| ||| ||| ||| |||

Db	6667	taaccacagatgacccatttttccacatgcttgggagagaggggttaccctcaatttc	6726
Q7	167	atgggaatgagtttggcattcc	189
Db	6727	atgggtaacgaggtatgctcttac	6749

```

RESULT 11
US-09-351-414-3
; Sequence 3, Application US/09351414
; Patent No. 6265199
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/351,414
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
;

```

```

?
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: zdm1t1 amino acid degenerate sequence
?
? FEATURE:
? NAME/KEY: variation
? LOCATION: (1)...(2088)
? OTHER INFORMATION: n is any nucleotide
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(2088)
? OTHER INFORMATION: n = A,T,C or G
US-09-351-414-3

```

Query Match	3.6%	Score 36.4	DB 4	Length 2088
Best Local Similarity	29.3%	Pred. No. 0.63		
Matches 60	Conservative 38	Mismatches 107	Indels 0	Gaps 0

QY 237 tgaatttgaaacacatgctttcttcacatgtaatgtaataatcctgttgcctcaa 296
 Db 1006 tgyathagagargaracnngnmgtnwscacawsmgmnaartlywsnartgywsnathyn 1065
 QY 297 ggaagaaagttaactcttacttacttgcagaatgatagatttcccaagaagccaccaaa 356
 Db 1066 gartacayagaycttlytncarimgnngnngnngcgtlytntlyeaayngnccnaacnaar 1125
 QY 357 ctcttccaaccggcaagaagtctctcccttgaaataacaatagttaataataatgcgcgct 416
 Db 1126 yltnttygarccnaacnargartgysgnaaygntatytngargcngnngnargartgcyagatgy 1185
 QY 417 agatttgatctctgtaagtttagct 441
 Db 1186 ganttycaygtngartgtaatgtaaygny 1210

```

RESULT 12
US-08-647-351B-1
; Sequence 1, Application US/08647351B
; Patent No. 5770368
;
; GENERAL INFORMATION:
; APPLICANT: De Leon, Ricardo
; APPLICANT: Rochelle, Paul
; TITLE OF INVENTION: Cryptosporidium Detection Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 S. Lake Avenue, 9th Floor
; CITY: Pasadena
;

```

```

Query Match          3.6%; Score 36; DB 1; Length 3607;
Best Local Similarity 55.6%; Pred. No. 1;
Matches    69; Conservative   0; Mismatches   55; Indels      0; Gaps      0;

Oy 477 cattatattctgatagaacataaaagtgttggtaagaagacacattgtttgtagt 536
      ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db 91 CATTTGTTTCATAAATATATACATATTGTGATTAGTCTGTAAAAAATATATTGATTGA 150
Oy - 537 tttagagcgctaacataaagtatcgttgagaggttgtgatcatcaataaatatcagt 596
      | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db 151 GAGGAGATCCATTACCTTTATTTTATTAAGAATTTTTATTAATAAAGTGATTTATT 210
      ||| |||| | |||| | |||| | |||| | |||| | |||| |

Oy 597 tttt 600
      |||| 
Db 211 TTTY 214

RESULT 13
US-09-177-249-5/c
Sequence 5, Application US/09177249
Patent No. 6229064
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegarl, Ramlin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
FILE REFERENCE: Development in Plants
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 5801
TYPE: DNA
ORGANISM: Arabidopsis sp.
FEATURE:
NAME/KEY: CDS

```

1 GENERAL INFORMATION:
2 APPLICANT: Saito, Shuji
3 APPLICANT: Ohkawa, Setsuko
4 APPLICANT: Saeki, Sakiko
5 APPLICANT: Ohsawa, Ikuroh
6 APPLICANT: Funato, Hiroho
7 APPLICANT: Iritani, Yoshikazu
8 APPLICANT: Aoyama, Shigemi
9 TITLE OF INVENTION: Takahashi, Kiyochihiro
10 TITLE OF INVENTION: NEW POLYPEPTIDE, DNA ENCODING THE
11 TITLE OF INVENTION: POLYPEPTIDE, RECOMBINANT VECTOR BEARING THE DNA AND
12 TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
13 NUMBER OF SEQUENCES: 51
14 CORRESPONDENCE ADDRESSES:
15 ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND &
16 ADDRESSEE: NAUGHTON
17 STREET: 1725 K Street, Suite 1000
18 CITY: Washington
19 STATE: DC
20 COUNTRY: USA
21 ZIP: 20006
22
23 COMPUTER READABLE FORM:
24 MEDIUM TYPE: Floppy disk
25 COMPUTER: IBM PC compatible
26 OPERATING SYSTEM: PC-DOS/MS-DOS
27 SOFTWARE: Patent In Release #1.0, Version #1.30
28 CURRENT APPLICATION DATA:
29 APPLICATION NUMBER: US/08/525,742
30 FILING DATE: 25-SEP-1995
31 CLASSIFICATION: 424
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: JP 05-074139
34 FILING DATE: 31-MAR-1993
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: JP 05-245625
37 FILING DATE: 30-SEP-1993
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: PCT/JP94/00541
40 FILING DATE: 31-MAR-1994
41 ATTORNEY/AGENT INFORMATION:
42 NAME: Mclelland, Le-Nhung
43 REGISTRATION NUMBER: 31,541
44 REFERENCE/DOCKET NUMBER: 950811
45 TELECOMMUNICATION INFORMATION:
46 TELEPHONE: 202-659-2930

```

; TELEFAX: 202-8870357
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..1038
; US-08-525-742-5

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```

Query Match          3.5%: Score 35.2; DB 2; Length 1945;
Best Local Similarity 47.7%: Pred. No. 1.3;
Matches 103; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

```

```

QY 384 ggaataacaatagatgataaagccgcgtagattgactgtgaagtttagctgt 443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1433 GGATTTAAACGGGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1492

QY 444 gctattacattccctcactagatcttatttgcatttattcttgatgaataatg 503
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1493 TTGAAAGCTGTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1552

QY 504 ttcttgaggaaagatcaacattgcttcttgtagttttagagcgttaacataagfatggt 563
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1553 GTTATCTGAATAGATTTAGAGTGTCTTATTTAGTTGATCAACAATACCATCGTTGCTTT 1612

QY 564 tgaagatgttgatcatataaataatcatgatttt 599
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1613 CATTAAGCTCAGTAAGTAATGATTTTCAATCTT 1648

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```

RESULT 15
US-09-193-562D-29
; Sequence 29, Application US/09193562D
; Patent No. 6309857
; GENERAL INFORMATION:
; APPLICANT: Pauli, Benedicht U.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
; FILE REFERENCE: Activated Chloride Channel-Adhesion Molecules
; CURRENT APPLICATION NUMBER: US/09/193,562D
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US/60/065,922
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 3418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-562D-29

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Query Match          3.4%: Score 34.2; DB 4; Length 3418;
Best Local Similarity 47.7%: Pred. No. 3.3;
Matches 133; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

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```

QY 340 tccaagagggccacaactctccaaccgcaaggtctcccttgaataatacaatagtt 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2630 tccatgaagccaatgacccctcagaggttccaacatgcacaagcaactaacttattc 2689

QY 400 atgataatggcgcgtagattgactgtgaagtttagctgtgtattatcattccctc 459
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2690 ctccaaggaaccagcagctcctgctcgggtaccaaatattctgcacatcgattggcaa 2749

QY 460 actagatcttattgagcattattcttgatgaatacatatgtttttaggaagatc 519
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2750 ttcttgattagcgtgaatttatctatatttatactagaataattatagaactcaaa 2809

QY 520 aacattgctttagtattttagtagaagcttaacataa---glatgtgttgagaattgtga 576
    ..

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```

Db 2810 ttcaatgtatatacactactggtgaacatttatttaaaatttaactaactattgt 2869
QY 577 tcattaaaataatgatgtttttgcaggagagatgcaga 615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2870 ctattataaagctcatatataataataaagtgaaagtaca 2908

```

Search completed: September 12, 2002, 08:13:33
Job time: 14870 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 12, 2002, 08:10:22 : Search time 3207.55 Seconds
(without alignments)
4212.078 Million cell updates/sec

Title: US-09-508-377-10_COPY_9500_10500

Perfect score: 1001

Sequence: 1 tccgacatagaacacatga.....ctggagacatagctttttt 1001

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estlro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_lun:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	199.4	19.9	465	12	A0690523 nbxb00820
2	136.4	13.6	650	10	BE427534 PSR153 I
3	133.2	13.3	244	10	BE591091 WHE0861_C
4	133.2	13.3	375	10	BE419958 WMS019.E6
5	133.2	13.3	499	10	BE517857 WHE0803_A
6	133.2	13.3	592	10	BE402623 CSB009H05
7	130	13.0	471	9	AV914376 AV914376
8	130	13.0	801	9	BE195628 HVSMEH008
9	130	13.0	825	10	BF065047 HV_CEB002
10	118.8	11.9	448	10	D48464 RICS14669A
11	117.4	11.7	743	10	BE414598 SCU011.E0
12	114.2	11.4	494	10	BE498533 WHE0971_G
13	114.2	11.4	688	9	AV944141 AV944141
14	114.2	11.4	692	9	AV921312 AV921312
15	114.2	11.4	728	10	BI948391 HVSMEI000
16	113.2	11.3	506	10	BG366889 HVSMEI000
17	110.6	11.0	832	9	BE196055 HVSMEH009

18	110.6	11.0	918	9	BE196057	BE196057 HVSMEH009
19	106	10.6	243	9	AA751373	AA751373 ISYS0039
20	98.4	9.8	651	10	BG526727	BG526727 63-11 Ste
21	96.4	9.6	279	10	BI072226	BI072226 C071P70U
22	96.4	9.6	372	10	BI069710	BI069710 C006P40U
23	95.6	9.6	565	9	A1795537	A1795537 HVSMEH009
24	95.4	9.5	731	10	BE602527	BE602527 HVSMEH009
25	92.8	9.3	548	9	AM258093	AM258093 68706BD07
26	91.2	9.1	168	10	BM259431	BM259431 952009B08
27	91.2	9.1	560	9	A1737162	A1737162 605010C06
28	91.2	9.1	583	9	A1737050	A1737050 605017B02
29	91.2	9.1	592	9	AM231887	AM231887 687060C09
30	91.2	9.1	612	9	AM061921	AM061921 687009B05
31	91.2	9.1	613	9	A1665623	A1665623 605013G06
32	91.2	9.1	615	9	A1759057	A1759057 605084D05
33	90.2	9.0	526	9	AM216035	AM216035 687050F06
34	90	9.0	433	10	BG551002	BG551002 sad3109.
35	90	9.0	582	10	BM309136	BM309136 sak55b02.
36	90	9.0	689	10	BI308555	BI308555 EST529965
37	89.6	9.0	595	9	A1833354	A1833354 605086C12
38	89	8.9	621	10	BG521671	BG521671 13-3 Stev
39	88.4	8.8	509	10	BG651974	BG651974 sad72810.
40	88.4	8.8	571	10	BI469105	BI469105 sai07609.
41	88.4	8.8	571	10	BI699680	BI699680 sai25909.
42	88.4	8.8	589	9	AM596011	AM596011 s196903.Y
43	86.8	8.7	601	9	A1993785	A1993785 701514536
44	85.4	8.5	184	9	AA751420	AA751420 ISYS0089
45	85.2	8.5	569	9	AV442128	AV442128 AV442128

ALIGNMENTS

RESULT 1
A0690523/c
LOCUS
DEFINITION nbxb008201lf CUGI Rice BAC Library Oryza sativa genomic clone
ACCESSION A0690523.1 GI:531691
VERSION A0690523.1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 465)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TATACGACTCATTATGCG
Class: BAC ends
High quality sequence stop: 177.
Location/Qualifiers
1..465
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nbxb008201lf"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBel08C11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those

BASE COUNT	163 a	86 c	93 g	123 t
ORIGIN				

```

Qy 75 ctcaactcttcgcatgtatgctgcatagcatatcataaagtcatcgcttltcaacca 134
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 459 CTTCAACACCTCGCATTTGATCGTGGATAGCATTAACAATAATGATTAGCGTTGTCAACA 400

```

Oy 195 agctcttaacaacattatgcatcctcgatgatgtgattacttacctgaatttgaaaccaty-c 2533

Db 339 AGGATTTTATTC-TCTTGCAATTGTACTAATTTTTATTGAAGCGTTTAAGCCACGAC 2811

Qy 314 attactctgcagaatgtagatattctccaagagggccacaactcttccaacgcgcaaa 373
||||| ||||||| ||||||| ||||||| ||| ||||||| |||
hb 226 ttttttaccttttcagagatgcattgattttttttccaaagcccccgcgcaaaatgctcttc 1672

QY 434 tttagctgtgctattacatccctcaactagatcttattgtgccatttattctgatga 493

DB 4 / ACACATGTCGTTAGATAAGATCACAGCTGCTTACGTGGG 1

VERSION	BE427534.1	GI:9425377
KEYWORDS	EST.	
SOURCE	bread wheat.	

REFERENCE
AUTHORS
1 (bases 1 to 650)
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier,
S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,

Cereals Group, John Innes Centre
Norfolk, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 452571 ext. 2587
Fax: 44 1603 502241
Email: paul.balley@bbsrc.ac.uk
International Trilicaceae EST Cooperative (ITEC)
<http://wheat.pw.usda.gov/genome>.

FEATURES	Location/Qualifiers
source	1. .650

Query Match	13.6%	Score 135.4	DB 10	Length 650
Best Local Similarity	98.7%	Pred. No. 2.4e-21		
Matches 148	Conservative 0	Mismatches 1	Indels 1	Gaps 1

QY 102 tagattacataaanaatgatacagctctgacacatggtttagtgytgaagctatccta 161

RESULT 3

ACCESSION	BE591091
VERSION	BE591091.1
KEYWORDS	GI:9846085 EST.
SOURCE	bread wheat.

AUTHORS Anderson, O. D., Chao, S., Choi, D. W., Close, T. J., Fenton, R. D., Han, P. S., Hsia, C. C., Kang, Y., Lazo, G. R., Miller, R., Rausch, C. J., Seaton, C. L. and Tong, J. C.

JOURNAL genomes - 20-45 DAP spike cdna library
COMMENT unpublished (2000)
Contact: Olin Anderson

Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stragene SK primer.

FEATURES

source

Location/Qualifiers

1..244
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0861_C09_F17"
/clone_lib="wheat 20-45 DAP spike cDNA library"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give phagescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 66 a 41 c 64 g 73 t

ORIGIN

Query Match

13.3%; Score 133.2; DB 10; Length 244;

Best Local Similarity 97.3%; Pred. No. 1.1e-20;

Matches 146; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 43 agagatgtatgatttcacgtcgtcgatag-gctcaactcttcgcatgctgagca 101

Db 86 AGCATATGATGATTTTCATGCTCTGTGATGACCTTCACCTCCGATTGATGCGCA 145

Qy 102 tagcatatacaaaatgacagcgtgtcaccaatgggttaggttggaagctatccta 161

Db 146 TAGCATTAACATAAATGATGACGCTTGTCACCATGGGTTAGTGGCAAGCTATCTTA 205

Qy 162 acttcattgggaatgagttgggcatcctg 191

Db 206 ACTTCATGGGAATGAGTTGGGCATCTCG 235

RESULT 4

BEA19958

LOCUS BEA19958 375 bp mRNA linear EST 24-JUL-2000

DEFINITION WMS019.E6R000101 ITEC WMS Wheat Scutellum library Triticum aestivum

CDNA clone WMS019.E6, mRNA sequence.

BEA19958

BEA19958.1 GI:9417804

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
1 (bases 1 to 375)

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier,
S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
Herrmann, R.G., Holton, T., Jacquemais, J.M., Jia, J., Joudrier, P.,
Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,
Pechioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shafitlou, M.,
Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)

JOURNAL

COMMENT

Contact: Schuch W

zeneca Wheat Improvement Centre, Norwich Research Park

Colney Lane, Norwich NR4 7UH UNITED KINGDOM

Tel: 44 1603 250 2600

Fax: 44 1603 250 699

Email: wolfgang.schuch@aguk.zeneca.com

International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.

FEATURES

source

Location/Qualifiers

1..375
/organism="Triticum aestivum"
/cultivar="Novosibirskaya 67"
/db_xref="taxon:4565"
/clone="WMS019_E6"
/clone_lib="ITEC WMS Wheat Scutellum library"
/tissue_type="scutellum callus"
/note="M13 Reverse sequencing primer used for 5' end of
clone."

BASE COUNT 107 a 70 c 89 g 108 t 1 others

ORIGIN

Query Match

13.3%; Score 133.2; DB 10; Length 375;

Best Local Similarity 97.3%; Pred. No. 1.2e-20;

Matches 146; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 43 agagatgtatgatttcacgtcgtcgatag-gctcaactcttcgcatgctgagca 101

Db 83 AGCATATGATGATTTTCATGCTCTGTGATGACCTTCACCTCCGATTGATGCGCA 142

Qy 102 tagcatatacaaaatgacagcgtgtcaccaatgggttaggttggaagctatccta 161

Db 143 TAGCATTAACATAAATGATGACGCTTGTCACCATGGGTTAGTGGCAAGCTATCTTA 202

Qy 162 acttcattgggaatgagttgggcatcctg 191

Db 203 ACTTCATGGGAATGAGTTGGGCATCTCG 232

RESULT 5

BE517857

LOCUS BE517857 499 bp mRNA linear EST 08-AUG-2000

DEFINITION WHE0803_A06_B11ZS wheat vernalized crown cDNA library Triticum

aestivum cDNA clone WHE0803_A06_B11, mRNA sequence.

BE517857

BE517857.1 GI:9741887

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
1 (bases 1 to 499)

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
genomes - Vernalized crown cDNA library
Unpublished (2000)

JOURNAL

COMMENT

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific

West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105355773

Fax: 5105355818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20

Seq primer: Stragene SK primer.

FEATURES

source

Location/Qualifiers

1..499
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0803_A06_B11"
/clone_lib="wheat vernalized crown cDNA library"
/tissue_type="Crown tissue of seedling"
/dev_stage="Five-week old seedling"
/lab_host="E. coli SOLR"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid, site_1: EcoRI, site_2: XhoI; Seeds were germinated and grown at 4 C for 5 weeks. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the T7 Close Lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson Lab (all other authors)."

BASE COUNT 149 a 91 c 121 g 138 t

Query Match 13.3%; Score 133.2; DB 10; Length 499;
Best Local Similarity 97.3%; Pred. No. 1.3e-20;
Matches 146; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Oy 43 aggatattgatattcattgctctgtag-gctcaactcttcgattgtagca 101
|||||
Db 105 AGGATATGATGATTTCATGGCTCTGGATAGACCTCAACCTCCGATTCGTGGCA 164
|||||
Oy 102 tagcatcataaataatgacagctgacacatggttgtagtaagctactta 161
|||||
Db 165 TAGCATTCATTAATAATGATCAGGCTTGACCATGGTTTAGTGGCAAGGCTATCTTA 224
|||||

Oy 162 actcatgggaatgattggtggacacctg 191
|||||
Db 225 ACTCATGGGAATGATGATTGGGCAATCCTG 254
|||||

RESULT 6
BE402623 592 bp mRNA linear EST 21-JUL-2000
LOCUS CSB009H05P990908 ITEC CSB Wheat Endosperm Library Triticum aestivum
DEFINITION cDNA clone CSB009H05, mRNA sequence.
ACCESSION BE402623
VERSION BE402623.1 GI:9362091
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae

REFERENCE 1 (bases 1 to 592)

AUTHORS

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.Y., McGuire, P., Ogihara, T., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
International Triticaceae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticaceae
Unpublished (2000)

JOURNAL

COMMENT
Contact: Appels R
Div. of Plant Industry, CSIRO
Canberra ACT 2601 AUSTRALIA
Tel: 61 62 465496
Fax: 61 62 465000
Email: rudiepi.csiro.au
International Triticaceae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
location/Qualifiers

FEATURES

source
1. 592
/organism="Triticum aestivum"
/cultivar="Wynna"
/db_xref="taxon:4565"
/clone_id="ITEC CSB Wheat Endosperm Library"
/tissue_type="endosperm"
/dev_stage="8-12 days post anthesis"
/lab_host="Escherichia coli SOLR"
/note="Vector: Lambda Zap/Bluscript; Site_1: XhoI; Site_2: EcoRI; Plants grown in Phytotron with 18C/13C

(day/night) 16 hour light. M13 Reverse sequencing primer used. 1.0 kbp average insert size."

BASE COUNT 164 a 116 c 144 g 167 t

Query Match 13.3%; Score 133.2; DB 10; Length 592;
Best Local Similarity 97.3%; Pred. No. 1.3e-20;
Matches 146; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Oy 43 aggatattgatattcattgctctgtag-gctcaactcttcgattgtagca 101
|||||
Db 6 AGGATATGATGATTTCATGGCTCTGGATAGACCTCAACCTCCGATTCGTGGCA 65
|||||
Oy 102 tagcatcataaataatgacagctgacacatggttgtagtaagctactta 161
|||||
Db 66 TAGCATTCATTAATAATGATCAGGCTTGACCATGGTTTAGTGGCAAGGCTATCTTA 125
|||||
Oy 162 actcatgggaatgattggtggacacctg 191
|||||
Db 126 ACTCATGGGAATGATGATTGGGCAATCCTG 155
|||||

RESULT 7
AV914376 471 bp mRNA linear EST 18-JAN-2002
LOCUS AV914376 K. Sato unpublished cDNA library, cv. Haruna Nijo
DEFINITION germination shoots Hardeum vulgare subsp. vulgare cDNA clone
bagg5011 5', mRNA sequence.
ACCESSION AV914376
VERSION AV914376.1 GI:18210153
KEYWORDS EST.
SOURCE Hardeum vulgare subsp. vulgare.
ORGANISM Hardeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae

REFERENCE 1 (bases 1 to 471)

AUTHORS

Sato, K., Saisyo, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
location/Qualifiers

FEATURES

source
1. 471
/organism="Hardeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="bagg5011"
/clone_id="K. Sato unpublished cDNA library, cv. Haruna Nijo germination shoots"
/tissue_type="shoots"
/dev_stage="germination"

BASE COUNT 138 a 81 c 116 g 135 t

Query Match 13.0%; Score 130; DB 9; Length 471;

Best Local Similarity 96.0%; Pred. No. 6.9e-20;
Matches 144; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Oy 43 aggatattgatattcattgctctgtag-gctcaactcttcgattgtagca 101
|||||
Db 100 AGGATATGATGATTTCATGGCTCTGGATAGACCTCAACCCCTCGATTCGTGGCA 159
|||||
Oy 102 tagcatcataaataatgacagctgacacatggttgtagtaagctactta 161
|||||
Db 160 TAGCATTCATTAATAATGATCAGGCTTGACCATGGTTTAGTGGCAAGGCTATCTTA 219
|||||

QY 162 acttcattggaatgagttgggcatctg 191
 Db 220 ATTTCATGGGAATGAGTTGGGCATCTCG 249

RESULT 8

LOCUS BE195628 801 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSMNH0089P20f Hordeum vulgare 5-45 DAP spike EST library
 HVCNMA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMNH0089P20f,
 mRNA sequence.

ACCESSION BE195628
 VERSION BE195628.2 GI:13188305
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 801)
 Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
 ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
 ,R.D., Close,S.J., Oates,R. and Main,D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex 5-45 DAP spike cDNA library
 Unpublished (2001)
 On Jun 26, 2000 this sequence version replaced gi:8707823.
 CONTACT: Wing RA
 CLEMSON UNIVERSITY GENOMICS INSTITUTE
 CLEMSON UNIVERSITY
 100 JORDAN HALL, CLEMSON, SC 29634, USA
 TEL: 864 656 7288
 FAX: 864 656 4293
 EMAIL: rwing@clmson.edu
 Total hg bases = 408
 Seq primer: AATTAACTCTCCTACTAAAGCG
 High quality sequence stop: 611.
 Location/Qualifiers
 1..801
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone_lib="HVSMNH0089P20f"
 /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
 HVCNMA0009 (5 to 45 DAP)"
 /tissue_type="5-45 DAP Spike"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP. Site.1: EcoRI; Site.2: XhoI;
 plants were grown in the greenhouse at the University of
 California, Riverside (Fenton, SJ Close, TJ Close). Whole
 spikes with awns trimmed were collected at 5, 10, 15, 20,
 30 and 45 DAP (Fenton). Total RNA was prepared from each
 pool, equal quantities of all six RNA pools were combined,
 poly(A) RNA was purified from the mixture, one primary
 unamplified cDNA library was made, and 1 million pfu were
 in vivo excised to give plasmid SK(-) cDNA phagemids
 (Choi) in the TJ Close lab at the University of California,
 Riverside. Phagemids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
 The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)."

BASE COUNT 220 a 146 c 198 g 236 t 1 others
 ORIGIN

Query Match 13.0%; Score 130; DB 9; Length 801;
 Best Local Similarity 96.0%; Pred. No. 7.6e-20;
 Matches 144; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 43 aggatgtatgatattcatgctctgtagatg-gctcaactcttcgcatgactgagca 101
 Db 291 AGGATGTATGATATTTCATGCGCTGTGATAGACCTTCAACCCCTGCATTGATCGGCA 350

QY 102 tagcatatcataaataagacagctgtccacatgggttagtggtagaagctatctta 161
 Db 351 TAGCATTAACATAAAGATGACGAGCTGTACCATGGGTTAGGTGGCAGGACTATCTTA 410

QY 162 acttcattggaatgagttgggcatctg 191
 Db 411 ATTTCATGGGAATGAGTTGGGCATCTCG 440

RESULT 9
 BF065047
 LOCUS BF065047 825 bp mRNA linear EST 23-OCT-2001
 DEFINITION HV_CEB0022L05f Hordeum vulgare seedling green leaf EST library
 HVCNMA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
 HV_CEB0022L05f, mRNA sequence.

ACCESSION BF065047
 VERSION BF065047.1 GI:10841686
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 825)
 Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
 Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
 ,D.W., Fenton,R.D., Oates,R. and Main,D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Blumeria infected incompatible (Mla6) seedling
 leaf cDNA library
 Unpublished (2001)
 CONTACT: Wing RA
 CLEMSON UNIVERSITY GENOMICS INSTITUTE
 CLEMSON UNIVERSITY
 100 JORDAN HALL, CLEMSON, SC 29634, USA
 TEL: 864 656 7288
 FAX: 864 656 4293
 EMAIL: rwing@clmson.edu
 Total hg bases = 594
 Seq primer: AATTAACTCTCCTACTAAAGCG
 High quality sequence stop: 732.
 Location/Qualifiers
 1..825
 /organism="Hordeum vulgare"
 /cultivar="C116151 (Mla6)"
 /db_xref="taxon:4513"
 /clone_lib="HV_CEB0022L05f"
 /clone_lib="Hordeum vulgare seedling green leaf EST
 library HVCNMA0005 (Blumeria challenged)"
 /tissue_type="seedling green leaf"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP. Site.1: EcoRI; Site.2: XhoI;
 C.I. 16151 (Mla6) plants were greenhouse grown in the R
 Wise lab at Iowa State University, Ames, IA; 7 day old
 green seedlings were challenged with isolate 5874 (AVR/Mla6
) of Blumeria graminis f. sp. hordei, and leaves were
 harvested 20 and 24 hr post-inoculation and snap frozen;
 uninoculated leaves were harvested 20 hr post-inoculation
 (Wei, Wise). In the TJ Close lab at the University of
 California, Riverside, total RNA was prepared from each
 sample pool, equal quantities of all three RNA pools were

combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give phleuescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)

BASE COUNT 220 a 167 c 212 g 226 t

Query Match 13.0% Score 130; DB 10; Length 825;
Best Local Similarity 96.0% Pred. No. 7.7e-20;
Matches 144; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 43 aggaatgatgatcttcagctcgtgatag-gctcaaccttcgcatgacgtgca 101
|||||
Db 59 AGGATATGTATGATTTATGCTGCTGGATAGACCTTCAACCCCTGCATTCGTGCA 118
|||||
Qy 102 tagcatcataaataatgatcagcttgcacacatggttgatgagtgatctctta 161
|||||
Db 119 TAGCATTTACATTAATATGATCAGGCTTGTCACCATGGGTTAGTGGCGAAGGCTATCTTA 178
|||||
Qy 162 attcatatggaatgagttggtgcatcctg 191
|||||
Db 179 ATTTCATGGAATGATGATTTGGGCTGCTG 208
|||||

RESULT 10

LOCUS D48464 448 bp mRNA linear EST 02-AUG-1995
DEFINITION R10S1665A Rice green shoot Oryza sativa cDNA, mRNA sequence.
ACCESSION D48464
VERSION D48464.1 GI:702173
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzoideae; Oryza.

REFERENCE 1 (bases 1 to 448)
AUTHORS Sasaki,T., Miyao,A. and Yamamoto,K.
TITLE Rice cDNA from callus 1995
JOURNAL Unpublished (1995)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@dr.affrc.go.jp, URL: <http://rtp.dna.affrc.go.jp/>.

FEATURES
source
1..448
/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone_id="Rice green shoot"
/note="Green shoot (8 days old)"

BASE COUNT 131 a 81 c 113 g 122 t 1 others
ORIGIN

Query Match 11.9% Score 118.8; DB 10; Length 448;
Best Local Similarity 91.3% Pred. No. 2.7e-17;
Matches 137; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 43 aggaatgatgatcttcagctcgtgatag-gctcaaccttcgcatgacgtgca 101
|||||
Db 45 AGGATATGTATGATTTATGCTGCTGGATAGACCTTCAACCCCTGCATTCGTGCA 104
|||||
Qy 102 tagcatcataaataatgatcagcttgcacacatggttgatgagtgatctctta 161
|||||
Db 105 TAGCATTTACATTAATATGATCAGGCTTGTCACCATGGGTTAGAGGCGAAGGCTATCTTA 164
|||||

Qy 162 attcatatggaatgagttggtgcatcctg 191
|||||
Db 165 ATTTCATGGAATGATGATTTGGGCTGCTG 194
|||||

RESULT 11
BE414598 743 bp mRNA linear EST 24-JUL-2000
LOCUS SCU011.E01.R990714 ITREC SCU Wheat Endosperm Library Triticum

DEFINITION aestivum cDNA clone SCU011.E01, mRNA sequence.
ACCESSION BE414598
VERSION BE414598.1 GI:9412444
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 743)
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Izzo,G.R., Lin,J.J., McGuire,P., Ogihara,T.,
Pechioni,N., Quailset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
Sorrells,M., Warburton,M. and Wenzel,G.
International Triticaceae EST Cooperative (ITREC): Production of
Expressed Sequence Tags for Species of the Triticaceae
Unpublished (2000)

JOURNAL Contact: Holton T
COMMENT Centre for Plant Conservation Genetics, Southern Cross University
PO Box 157, Lismore NSW 2480 AUSTRALIA
Tel: 61 2 6620 3409
Fax: 61 2 6622 2080
Email: tholton@scu.edu.au
International Triticaceae EST Cooperative (ITREC)
<http://wheat.pw.usda.gov/genome>.

FEATURES
source
1..743
/organism="Triticum aestivum"
/cultivar="Wynna"
/db_xref="taxon:4565"
/clone="SCU011.E01"
/clone_id="ITREC SCU Wheat Endosperm Library"
/tissue_type="endosperm"
/note="Vector: Bluescript II SK(-)"

BASE COUNT 195 a 159 c 178 g 190 t 21 others
ORIGIN

Query Match 11.7% Score 117.4; DB 10; Length 743;
Best Local Similarity 95.3% Pred. No. 6.2e-17;
Matches 121; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 65 tctgataggttcaaccttcgcatgatactggtgcatagcatcataaataatgacag 124
|||||
Db 114 TCGGACAGAGCTTCAACCTCCGATTCATGATGTCGATTCATTAATAATATCAGG 173
|||||
Qy 125 ctgtcacacatggttgatggtggaaggtcatcttaactcatggaatgagttgg 184
|||||
Db 174 CTGTGACACATGGGTTTAGTGTTGAGGCTATCTTAACCTTCATGCGAATGATTTGGG 233
|||||

OY 185 catcccg 191
|||||
Db 234 CATCCG 240

RESULT 12

BE498533
LOCUS BE498533 494 bp mRNA linear EST 04-AUG-2000
DEFINITION WHE0971.G03_M05ZS wheat pre-anthesis spike cDNA library Trilicium
aestivum cDNA clone WHE0971.G03_M05, mRNA sequence.

ACCESSION BE498533
VERSION BE498533.1 GI:9697150
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Trilicium aestivum

REFERENCE
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
CONTACT: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
1. 494

TITLE
JOURNAL
COMMENT

FEATURES
source
/organism="Trilicium aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0971.G03_M05"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="T. COIL SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pluescript
phagemids in the IV Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 129 a 106 c 135 g 124 t
ORIGIN

Query Match 11.4%; Score 114.2; DB 10; Length 494;
Best Local Similarity 97.5%; Pred. No. 3, 2e-16;
Matches 116; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 883 gttatgacatctgagcaccagatgtttcaaggaacatgaggaataagtgatcat 942
|||||
Db 85 GTTATGACATCTGAGACACAGTATGTTTCACGAAACAGAGAGATAGGTGATCAT 144

OY 943 ccccaaaaaggagattgttattgtttcaactccactgaggaataagctttttg 1001
|||||
Db 145 CTTCGAAAGAGGAGATTGTGTTTTCACCTTCACGAGCAATAGCTTTTGG 203

RESULT 13

AV944141/c
LOCUS AV944141 688 bp mRNA linear EST 18-JAN-2002
DEFINITION AV944141 K. Sato unpublished cDNA library, strain H602 adult,
heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone ban20e24 3', mRNA sequence.

ACCESSION AV944141
VERSION AV944141.1 GI:18239938
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum

REFERENCE
AUTHORS Sato,K., Saisho,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1. 688

FEATURES
source
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="bah20e24"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
180 c 145 g 177 t 2 others

BASE COUNT 184 a 180 c 145 g 177 t 2 others
ORIGIN

Query Match 11.4%; Score 114.2; DB 9; Length 688;
Best Local Similarity 97.5%; Pred. No. 3, 4e-16;
Matches 116; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 883 gttatgacatctgagcaccagatgtttcaaggaacatgaggaataagtgatcat 942
|||||
Db 612 GTTATGACATCTGAGACACAGTATGTTTCGAAACATGAGAGATAGGTGATCAT 553

OY 943 ccccaaaaaggagattgttattgtttcaactccactgaggaataagctttttg 1001
|||||
Db 552 CTTCGAAAGAGGAGATTGTGTTTTCACCTTCACGAGCAATAGCTTTTGG 494

RESULT 14
LOCUS AV921312 692 bp mRNA linear EST 18-JAN-2002
DEFINITION AV921312 K. Sato unpublished cDNA library, cv. Haruna Nijo
germination shoots Hordeum vulgare subsp. vulgare cDNA clone
bags23a09 3', mRNA sequence.

ACCESSION AV921312
VERSION AV921312.1 GI:18217091
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE
AUTHORS Sato,K., Saisho,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES
 source Location/Qualifiers

1. 692
 /organism="Hordeum vulgare subsp. vulgare"
 /cultivar="Haruna Nijo"
 /db_xref="taxon:112509"
 /clone="bags23a09"
 /clone_id="K. Sato unpublished cDNA library, cv. Haruna Nijo germination shoots"
 /tissue_type="shoots"
 /dev_stage="germination"
 BASE COUNT 183 a 184 c 147 g 176 t 2 others
 ORIGIN

Query Match 11.4%; Score 114.2; DB 9; Length 692;
 Best Local Similarity 97.5%; Pred. No. 3.4e-16;
 Matches 116; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 883 gttttagacatctgagcaccagatgtttcaaggaacatgagaagaatgagatcat 942
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 580 GTTTATGACATCTGAGCACCACATATGTTCTCGAAACATGAGAGATAGGTATCAT 521
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 943 cctcaaaagagagattgtgattttttcaacttcacactgagacaatagctttttg 1001
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 520 CTTGCAAGAGAGATTGGTATTGTTTTCACCTCCACGAGCAATAGCTTTTGG 462

RESULT 15
 BI948391 728 bp mRNA linear EST 19-OCT-2001
 LOCUS HVSMEL0009F19f Hordeum vulgare spike EST library HVCDNA0012
 DEFINITION (Fusarium infected) Hordeum vulgare cDNA clone HVSMEL0009F19f, mRNA
 sequence.
 ACCESSION BI948391
 VERSION BI948391.1 GI:16288749
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 ; Triticeae; Hordeum.
 1 (bases 1 to 728)
 Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinemann, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main, D.

TITLE Development of a genetically and physically anchored EST resource for barley genomics: Fusarium infected Morex spike cDNA library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 639
 Seq primer: AATTAACTCTCCTAAAGG
 High quality sequence stop: 680.

FEATURES
 source Location/Qualifiers

1. 728
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEL0009F19f"
 /clone_id="Hordeum vulgare spike EST library HVCDNA0012 (Fusarium infected)"
 /tissue_type="Spike"
 /lab_host="TJC121"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heineman). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/99pages/bgn/31/cover.html>)

BASE COUNT 192 a 151 c 188 g 192 t 5 others
 ORIGIN

Query Match 11.4%; Score 114.2; DB 10; Length 728;
 Best Local Similarity 97.5%; Pred. No. 3.4e-16;
 Matches 116; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 883 gttttagacatctgagcaccagatgtttcaaggaacatgagaagaatgagatcat 942
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 62 GTTTATGACATCTGAGCACCACATATGTTCTCGAAACATGAGAGATAGGTATCAT 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 943 cctcaaaagagagattgtgattttttcaacttcacactgagacaatagctttttg 1001
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 122 CTTGCAAGAGAGATTGGTATTGTTTTCACCTCCACGAGCAATAGCTTTTGG 180

Search completed: September 12, 2002, 08:10:33
 Job time: 16663 sec
